

## STIC Search Report Biotech-Chem Library

## STIC Database Tracking Number: 164274

TO: Richard Schnizer

Location: rem/2D30/2C18

Art Unit: 1635

Thursday, September 08, 2005 Case Serial Number: 09/910432 From: Barb O'Bryen

**Location: Biotech-Chem Library** 

Remsen 1a69

Phone: 571-272-2518

BOB

barbara.obryen@uspto.gov

Search Notes	The same of the sa	A STATE OF THE STA	Andrew Control of the
·	•		
·			•



This Page Blank (uspto)

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

This Page Blank (uspto)

```
drosophila
drosophila
caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                     oryza sativ
oryza sativ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lycopersico
drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oryza sativ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasmodium
drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          triticum ae
triticum ae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rhizobium m
                                                                                                                                                                                                                                                                                                                                                                          Q69xv3 oryza sativ
                                                                                                                                                                                                                                                                                                                                                                                           oryza Bativ
                                                                                                                                                                                                                                                                                                                                                                                                                                        burkholderi
caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            drosophila
drosophila
                                                                                                                                                                                                                                                                                                                                                                                                             caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gallus gall
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ectocarpus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drosophila
                                                 7, 2005, 12:47:19; Search time 112.5 Seconds (without alignments) 232.143 Million cell updates/sec
                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 095nu6
095np2
07yxc8
                                                                                                                                                                                                                                                                                                                                                                                          085215
027294
027294
075hg8
062fe6
0642fe
084352
095w2
09837
09837
09837
098116
09116
09117
09117
09117
09117
09117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09gp44
092p87
095ux3
095ux5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      095nr6
                                                                                                                                                                      1612378
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                    1612378 seqs, 512079187 residues
                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                      Q62FE6
Q9UZU0
Q8QKX8
Q95UW6
Q43522
Q95UX2
FXGA_CHICK
Q915N6
Q69T79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9GRW7
FBRL DROER
O15647
FBRL DROME
                                                                                                                                                                                                                                                                                                                                                                                065514
Q85215
CAZ DROME
Q18444
GRP1 ORYSA
Q754G8
                                  - protein search, using sw model
                                                                                                                                                                                                                                    Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q75QNB
Q95UX4
Q95NR6
Q9GP44
Q92P87
                                                                                                                                                                                                                                                                                                                                                                        Q69XV3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q95NU6
Q95NP2
Q7YXC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0950X5
                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                               1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                            Maximum Match 100%
                                                                                                                                                                                       seq length: 0
seq length: 200000000
                                                                                                                                                                                                                  Post-processing: Minimum Match 08
                                                                                      US-09-910-432-19
                                                                                                                                                                                                                                                                                                                                              Query
Match Length DB
                                                                                                                                                                                                                                                     UniProt_03:*
                                                   September
                                                                                                                         BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197
197
196
196
                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                        236.5
223
209.5
206.5
206.5
206
203
203
203
203
203
                                                                                                                                                                                                                                                                                                                                                                                                                                                       201.5
201
201
201
199
198.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198
198
197.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195.5
195.5
195.5
195.5
195
195
195
195
195
                                                                                                Perfect score:
                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198
                                                                                                                                                                                       Minimum DB Maximum DB M
                                 OM protein
                                                                                                        Sequence:
                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                      Database
                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                     Title:
                                                                                                                                                                                                                                                                                                                                              Result
                                                                                                                                                                                                                                                                                                                                                        Š.
```

[2] SEQUENCE FROM N.A.

Q7xjp7 arabidopsis 024184 oryza sativ 069up6 oryza sativ 061519 plasmodium 065450 arabidopsis Q7pxr0 anopheles g Q92nu7 rhizobium m Q92nu7 rhizobium m Q93424 caenorhabdi Q94Q2 oryza sativ Q9sih2 arabidopsis Q9418 drosophila 042403 gallus gall P26968 tenebrio mo		update) on update) . protein.	; Trache	chromosome 6, PAC DBJ databases. :F649 CRC64;	; DB 2; Length 321; .1e-12; es 0; Indels 9; Gaps 1; GGGGGGGGGGGG 51 GGGGGGGGGGGG 142	e) ite) yyta; Tracheophy se eudicots; ro	Brandt A., Duesterhoeft A., Mewes H.W., Mayer K., DJ databases.
65 2 Q7XJP7 65 2 024184 88 2 029186 88 2 069UP6 96 2 065450 70 2 Q7PXR0 70 2 Q7PXR0 96 2 Q8RUS0 85 2 Q93424 85 2 Q942Q2 85 2 Q942Q2 85 2 Q942Q2 85 2 Q942Q2 85 2 Q942Q2 86 2 045Q2 87 2 Q942Q2 88 2 Q942Q2 89 1 AC22_TENMO	ALIGNMENTS RY; PRT; 321 AA.	1. 28, Created) 1. 28, Last sequence update) 1. 28, Last annotation update cell wall structural protein a cultivar-group).	Yamamoto K.;	(GA3) genomic DNA, the EMBL/GenBank/DL .1; 5 MW; DD83382025B2	ore 236.5 ed. No. 7 Mismatch RDDRRQRRR	RT; 221 ated) t sequenc t anotat t t annotat t t anotat c trophyta; cophyta; udicotyla; icaceae;	Braun M., Holzer E., Br., Heijnen L., Vos P., Me to the EMBL/GenBank/DDBJ
32 194.5 65.3 106 33 194.5 65.3 165 34 194.5 65.3 1088 35 194.5 65.3 2359 36 194.5 65.3 2359 37 193.5 64.9 170 38 193.5 64.9 236 40 192.5 64.6 385 41 192.5 64.6 255 42 191.5 64.4 255 43 191 64.1 239 44 191 64.1 239	SULT 1 9XV3 Q69XV3 PRELIMINARY	Q69XY3; 25-OCT-2004 (TrEMBLrel. 25-OCT-2004 (TrEMBLrel. 25-OCT-2004 (TrEMBLrel. Putative glycine-rich c Name-P0040H10.37; Oryza sativa (japonica	Eukaryota; Viridiplanta Spermatophyta; Magnoliop) Ehrhartoideae; Oryzeae; (NEI_TaxID=39947; [1] SEQUENCE FROM N.A. Sasaki T., Matsumoto T.,	"Oryza sativa nipponbare(GA clone:PO040H10."; Submitted (APR-2001) to the EMBL; AP003539; BAD35374.1; SEQUENCE 321 AA; 28605 M	Query Match Best Local Similarity 82.4%; Pr. Matches 42; Conservative 0; 1 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	SULT 2 5514 O65514 O65514 01-AUG-1998 (TEMBLre- 01-AUG-1998 (TEMBLre- 01-AUG-1998 (TEMBLre- 05-AUG-1998 (TEMBLre- 05-AUG-1998 (TEMBLre- Putative glycine-rich Name-F23E13.120; Syno Arabidopsis thaliana Evaryota, Viridiplani Spermatophyta; Wagnoli Spermatophyta; Wagnoli Spermatophyta; Magnoli Spermatophyta; Magnoli Spermatophyta; Magnoli Spermatophyta; Magnoli Spermatophyta; Magnoli	NCB. TAXIDES/UZ; [1] SEQUENCE FROM N.A. Bevan M., Hilbert H., E Hohelael J., Jesse T., Schueller C.; Submitted (MAR-1998) tc [2] SEQUENCE FROM N.A.
	RESULT Q69XV3 ID Q	AC DT DE GN OS	S S S S S S S S S S S S S S S S S S S	RT RT DR SQ	δ <sup>a</sup> <sup>w</sup> λ		R R R R R R R R R R R R R R R R R R R

```
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GGGGGGGGGGRGRDDRRQRRRGGG 34
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton Il L.L., Taikrin T., Kim M., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.; Ouackenbush J., Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ĠĠĠĠĠĠĠĠĠĠĠĠDVĠĠDĠĠĠĠĠĎĠ-----NVĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 209.5; DB 2; Length 329;
Pred. No. 1e-09;
0; Mismatches 4; Indels 9
                                                         SEQUENCE FROM N.A.
Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                       Length 221;
                                                                                                                                                                                                                                                                                                                                                                     74.8%; Score 223; DB 2; Length 221
55.8%; Pred. No. 6.1e-11;
iive 1; Mismatches 7; Indels
EU Arabidopsis sequencing project;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022141; CAA18129.1; -.
EMBL; AL161589; CAB80294.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AC091332, AA038820.1; -. Gramene; Q85215; -. Hypothetical protein. SEQUENCE 329 AA; 33756 MW; 0530227C1F442C71 CRC64;
                                                                                                                                                                                                                                                                                                                    11228; EGGSHELL.
221 AA; 20344 MW; DE8DAE2E2C57A9F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Last sequ
01-JUN-2003 (TrEMBLrel. 24, Last anno
Hypothetical protein OSJNBa0078A17.2.
Name-OSJNBa0078A17.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                               PIR, T04592, T04592.
InterPro, IPR002952; Eggshell.
PRINTS; PR01228; EGGSHELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 GGGGGGGGGGGGGG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 GGGGGGGGGGGG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 70.3%;
1 Similarity 75.5%;
40; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 55.8
Matches 43, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGGGGGGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                            PRINTS; PI
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buell R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148
                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    085215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
1085215
10 0452
AC 0852
AC 0852
DT 01-J
DT 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
```

RESULT 4

```
Manualides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gacayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R. Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
R.A. Bardon R.C., Rogers Y.-H.C., Blazei R.G., Champe M., Pfeiffer B.D.,
R.A. Bardon R.C., Ragers Y.-H.C., Blazei R.G., Champe M., Pfeiffer B.D.,
R.A. Ballew R.M., Baxendale J., Bayraktargolu L., Basaley E.M.,
Beeson K.Y., Benco P.V., Berman B.P., Bhandari D., Bolshakov S.,
R. Borkova D., Botchan M.R., Bouck J., Brokstein P., Bottier P.,
R. Cherry J.M., Cawley S., Dahlke C., Davenpour L.B., Davies P.,
R. Dodon K., Doup L.E., Downes M., Dugan-Rocha S., Pleists R.N.,
R. Dodon K., Doup L.E., Downes M., Dugan-Rocha S., Rleischmann W.,
R. Dodon K., Doup L.E., Downes M., Davan P., Herris M., Gabriellan A.E., Gargella G.Z., Glasser K.,
R. Dodon K., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
R. Dodon K., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
R. Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kerlum K.A.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kerlum K.A.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Metrei B., McInton T.C., Noriecd M.P., Morherson D.,
Reknin W. Matton B., McInton M., Moleson D.L.,
Relson D.R., Nelson K.A., Murphy L., Wurzhy D.M., Purl V., Resee M.G.,
Raber B.C., Siden-Kiamo G.S., Pan S., Pollard J., Wang X.,
Reinert K., Tector C., Turner R., Venter E., Wang X.,
Williams S.M., Woodage T., Saunders R.D.C., Scheeler F., Shen H.,
Raber X., Tector C., Turner R., Venter E., Wang X., Zhu R., Shen R.,
Raber R., Tector C., Turner R., Venter E., Wang X., Zhu X., Smith H.O.,
Raber R., Tector C., Turner R., Venter E., Wang X., Zhu X., Smith H.O.,
Raber R., Spradling A.C., Standers R.D.C., Scheeler F., Saunders R.A.,
Raber R., Shore R.W., Rubin G.M., Venter E., Stan S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS A AND B), FUNCTION, SUBCELLULAR LOCATION, DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stolow D.T., Haynes S.R., "Cabeza, a Drosophila gene encoding a novel RNA binding protein, shares homology with EWS and TLS, two genes involved in human sarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immanuel D., Zinszner H., Ron D.;
Association of SARFH (sarcoma-associated RNA-binding fly homolog)
with regions of chromatin transcribed by RNA polymerase II.";
Mol. Cell. Biol. 15:4562-4571(1995).
CAZ DROME STANDARD; PRT; 399 AA.
Q27294; Q24445; Q8T3M2; Q9VXI4;
16-OCT-2001 (Rel. 40, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
25-JMA-2005 (Rel. 46, Last annotation update)
RNA-binding protein cabeza (Sarcoma-associated RNA-binding fly
                                                                                                                                                                                                                                                                                                                                                       Name=caz; Synonyms=SARFH; ORFNames=CG3606;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM A), AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 23:835-843(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95349623; PubMed=7623847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95223793; PubMed=7708500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Canton-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Canton-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Formation.
```

m

```
1 GCGCCCCG-----GCGCGCGCGCGCCCCCCDDRRQRRRCCCCCCCC----CCCCCCCCC 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                   RNA-binding (RRM).
RanbP2-type.
Missing (in isoform A).
/FIId=VSP 005778.
PNY -> LFI (in Ref. 4).
H -> P (in Ref. 1, 2 and 6).
Missing (in Ref. 1, 2 and 6).
G -> GNGGGGG (in Ref. 1, 2 and 6).
D -> E (in Ref. 6 and 7).
DGGPWRNDGG -> WNQERRWS (in Ref. 6).
                                                                                                                                                                                                                                                                                                                                         Alternative splicing; Metal-binding; Nuclear protein; RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.3%; Score 206.5; DB 1; Length 399; 68.9%; Pred. No. 2.1e-09; ive 0; Mismatches 2; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Du Z., Le T.T.;
"The sequence of C. elegans cosmid C34D4.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38839 MW; 3001FC96BDD6FDCA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein C3414.11,
Name=C34D4.11; ORFNames=C34D4.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 136 AA.
  EMBL; AY094763; AAM11116.1; ALT_SEQ
                                                                                    HSSP, 095218; INOZ.
FlyBase; FBGH0011571; caz.
InterPro; IPR0000504; RNA rec mot.
InterPro; IPR001876; Znf_RanGDP.
Pfam; PF00076; RRM_1; 1.
Pfam; PF00641; zf-RanBP; 1.
                                                                                                                                                                                                                                                                   PROSITE; PS50102; RRM; 1.
PROSITE; PS01358; ZF RANBP2 1; 1.
PROSITE; PS50199; ZF_RANBP22; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                       EMBL; BT004875; AAO45231.1;
EMBL; M15765; AAA70425.1; -.
PIR; S54729; S54729.
                                                                                                                                                                                                                         SMART; SM00360; RRM; 1.
SMART; SM00547; ZnF_RBZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41
92
109
254
278
393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                       393
206
304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WormBase Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 G 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 G 49
                                                                                                                                                                                                                                                                                                                                                                  Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                    FING
                                                                                                                                                                                                                                                                                                                                                                                       OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q18444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      018444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                     GENOME REANNOTATION, AND ALTERNATIVE SPLICING.
MEDLINE=22426659; Pubmed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., NJ., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                    STRAIN=Berkeley; TISSUE-Embryo;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R.A., Gonzalez M., Guarin H., Kronmiller B., Li P.W., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J.M., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haynes S.R., Rebbert M.L., Mozer B.A., Forquignon F., Dawid I.B.; "Pen repeat sequences are GGN clusters and encode a glycine-rich domain in a Drosophila cDNA homologous to the rat helix destabilizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note-No experimental confirmation available;
TISSUE SPECIFICTY: Ubiquitous. Enriched in the brain and central nervous system during embryogenesis. Enriched in the adult head. Embryos contain both isoforms A and B, whereas later in development (heads and torses) only isoform B is detected. DEVELOPMENTAL STAGE: Expressed in the developing embryo from the earliest stages of cellularization and is subsequently found in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Nati. Acad. Sci. U.S.A. 84:1819-1823(1987).
-!- FUNCTION: May participate in a function common to the expression of most genes transcribed by RNA polymerase II.
-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                              "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  many cell types.

MISCELLANEOUS: 'Cabeza' means 'head' in Spanish.
SIMILARITY: Belongs to the RNP TET family.
SIMILARITY: Contains 1 RanBP2-type zinc finger.
SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-1988) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                            Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=027294-2; Sequence=VSP 005778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q27294-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Oregon-R;
MEDLINE=87175568; PubMed=3031652;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE003501; AAF48578.2; -. AE003501; AAN09389.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 212-261 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U13178; AAA86955.1; -.
EMBL; L37083; AAC41563.1; -.
Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 39-404 FROM N.A.
                                                                                                                                                                                                                                                                     systematic review.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Oregon-R;
                                                                                                                                                                                                                           Lewis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haynes S.R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.";
```

EMBL;

17; Gaps

```
Query Match
Best Local Similarity 72.5%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=ssb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                      Q75HG8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q62FE6
                                                                                                                                                                                                         RESULT 7
Q75HG8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
Q62FE6
                                                                                                                                      셤
                                                                                              à
                                                                                                                                                                                                                                                                             ACCOCCOS DATE RANGE OF THE READ OF THE REA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycine-rich cell wall structural protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A novel glycine-rich cell wall protein gene in rice.";
Plant Mol. Biol. 16:189-1981(1991).
-!- FUNCTION: Responsible for plasticity of the cell wall (Potential).
-!- SUBCELLULAR LOCATION: Cell wall (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (Rice).
Wkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 206; DB 2; Length 136;
Pred. No. 9.2e-10;
0; Mismatches 13; Indels
Waterston R.; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                               Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 136 AA; 12294 MW; F72778C4EA5649B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (Tyr-rich).
E36CE31C3650AC9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Glycine-rich cell wall structural protein 1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat; Signal; Structural protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gly-rich.
R2 (Tyr-rich).
R2 (Tyr-rich).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                 WormBase; WBGene00016403; C34D4.11.
WormPep; C34D4.11; CE17505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. Indica / IR36;
MEDLINE=91370862; PubMed=1716496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 R
13536 MW;
                                                                                                                                                                                                                                                 Submitted (SEP-2004) to the 1
EMBL; U58755; AAB00696.1; -.
PIR; T29282; T29282.
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 74.5%;
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X53596; CAA37665.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159
62
99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S13385; KNRZG1.
                                                                                                                                                                                                                            WormBase Consortium;
                                                                                         STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                             SEQUENCE FROM N.A.
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                         STRAIN-Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gramene; P25074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lei M., Wu R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell wall; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
SEQUENCE
                                                                                                               Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   유
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ATCC 23344;
Nierman W.C., De6hazer D., Kim H.S., Tettelin H., Nelson K.E.,
Feldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C.,
Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
Mohammoud Y., Nelson W.C., Radune D., Romero C.M., Sarria S.,
Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overcon Il L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Heiao J., Blunt S., Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Wang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraeer C.M.; Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Putative prohibitin.
Name-OSJNBa0024F18.27;
Oryza sativa (japonica cultivar-group).
Eukaryota, Viridplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                      109 dsaddadadadadasaQasdsgrayayakdadadadadadadadadasa 159
                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cedecedecedes cedecedes ce
                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 165;
                                                                                          13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buell R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59192 MW; 34C1EC87BB3CA297 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 68.3%; Score 203.5; DB 2; Best Local Similarity 72.5%; Pred. No. 4.7e-09; Matches 37; Conservative 0; Mismatches 3;
Score 206; DB 1;
Pred. No. 1.1e-09;
1; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 551 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burkholderia mallei ATCC 23344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burkholderiaceae; Burkholderia.
NCBI_TaxID=243160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single-strand binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001107; Band 7. Pfam; PF01145; Band 7; 1. SMART; SMO0244; PHB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AC135594; AAR89849.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORFNames=BMA3093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           551 AA;
```

```
RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                        116 GGGGGGGGGGGGDDGGYGGGGGGGGYDMERGGGGGRASGGGGAGARSGGGGGGGGG 175
                                                                                                                                          1 GGGGGGGGGG--GGGGGGGGGRGDDRRQRRRGGGGG----GGGG-----GGGGGGGGG
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 dededecesyasseconeceses p. ---rpresweseses reveses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51
                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4,
Zhou L., Fraser C.M.;
"Structural flexibility in the Burkholderia mallei genome.";
Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).
EMBL; CP000010; AAD48078.1; -.
SEQUENCE 199 AA; 19605 MW; 39022C03692C8D89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome sequence of the nematode C.elegans: A platform for
                                                                                    68.1%; Score 203; DB 2; Length 19
68.9%; Pred. No. 2.2e-09;
ive 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McMurray A.A.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL117204; CABSS137.1; -.
PIR; T31503; T31503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO1948; UANUXFACTOR.
SWART; SM00360; RRM; 1.
SMART; SM00356; ZnF C3H1; 2.
PROSITE; PS50102; RRM; 1.
Hypothetical protein.
SEQUENCE 285 AA; 30856 MW; E2B932629653C040 CRC64;
                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 203; DB 2
Pred. No. 3e-09;
0; Mismatches
                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MormBase; WBGene00006698; uaf-2.
WormPep; Y116A8C.35; CE23341.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR009106; CART_C.
InterPro; IPR000504; RNA_rec mot.
InterPro; IPR001945; U2 small.
InterPro; IPR000571; Znf_CCCH.
Pfam; PP00076; RRM 1; 1.
Pfam; PF00642; zf-CCCH; 2.
                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein Y116A8C.35.
Name=uaf-2; ORFNames=Y116A8C.35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.1%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998)
                                                                                 Query Match
Best Local Similarity 68.9
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IntAct; Q9U2U0; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6239;
                                                                                                                                                                                                                             G 176
                                                                                                                                                                                                   51 G 51
                                                                                                                                                                                                                             176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                   090200
                                                                                                                                                                                                                                                                  a
    SRRRS
                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
```

```
1;
                                                                                                                                                                                                                                                                             STRAIN=ESV-1;
Delarroque N., Bothe G., Pohl T., Knippers R., Mueller D.G., Boland W., Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF204951; AAF28325.1; -.
SEQUENCE 698 AA; 74035 MW; C7638DDB922E0D50 CRC64;
                                                                                                                                                                          MEDILINE=2019171; PubMed=10725207; DOI=10.1006/viro.2000.0225;
Delaroque N., Wolf S., Muller D.G., Knippers R.;
"Characterization and immunolocalization of major structural proteins in the brown algal virus EBV-1.";
Virology 269:148-155(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                              Name-OFF 144;
Ectocarpus siliculosus virus.
Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phaeovirus.
                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                               67.6%; Score 201.5; DB 2; Length 698; ilarity 68.4%; Pred. No. 8.2e-09; Conservative 0; Mismatches 3; Indels 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila ezoana (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.4%; Score 201; DB 2; Length lb. 77.1%; Pred. No. 2.7e-09; ... ... ... ... 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=E20;
Huttunen S., Vieira J., Hoikkala A.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AV0125600; AAG48870.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 AA; 15708 MW; 28A68346D17AB988 CRC64;
                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
 Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ž
                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC_2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No on or off transient A (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FlyBase; FBgn0046740; Dezo\nonA.
NON TER
                     01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-OCT-2003 (TrEMBLrel. 25, BSV-1-144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 77.1
Matches 37; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161
                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI TaxID=47313;
                                                                                                                                                                  STRAIN=ESV-1
                                                                                                                                                                                                                                                                                                                                                                                           39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=nonA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON TER
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Q8QKX8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q95UW6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      095UM6
                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
```

2

φ

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                   ---- 6GGGGGGGGGRDRNRGSRGGGGGGGGNS 115
their target genes.
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- DEVELOPMENTAL STAGE: Can be detected in regions including primordial retina and neuroepithelium by embryonic day 2 (E2). At E3, expressed in the temporal retina and associated pigment epithelium as well as in part of the diencephalon, and at E7 is expressed in retinal ganglion cells. Levels begin to decline from E4 and almost disappear by E10.
-!- SIMILARITY: Contains 1 fork-head domain.
                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=White leghorn; TISSUE=Retina; MEDLINE=96338226; PubMed=8757134; DOI=10.1038/382632a0; Yusas a J., Hirano S., Yamagata M., Noda M.; Yusas projection map specified by topographic expression of transcription factors in the retina."; Nature 382:632-632 (1996).

-I- FUNCTION: May determine the nasotemporal axis of the retina, and consequently specify the topographical projection of the retinal ganglion-cell axons to the tectum by controlling expression of
                                                                                                                                                                                                                                            T5-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Forkhead box protein GlA (Forkhead-related protein FKHL2)
(Transcription factor BF-2) (Brain factor 2) (BF2) (CBF-2) (Anne-FOXGIA; Synonyms-FKHL2, HFHBF2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, 063245; 2HDC.
InterPro; IPR001766; TF_Fork_head.
InterPro; IPR009058; Wing hlx_DNA_bnd.
Pfam; PF00250; FORKHEAD.
PRODM; PR000053; FORKHEAD.
ProDom; PR000425; TF_Fork_head; 1.
PROSITE; PS00657; FORK_HEAD_1; 1.
PROSITE; PS00659; FORK_HEAD_2; 1.
PROSITE; PS00659; FORK_HEAD_2; 1.
PROSITE; PS00639; FORK_HEAD_2; 1.
PROSITE; PS000639; FORK_HEAD_3; 1.
                                                                                                                                                                                                              440 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poly-Arg.
Poly-Glu.
Poly-Gly.
Poly-Ala.
Poly-Gly.
                                     67 gegegegegegegegegege
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U47276; AAB08467.1; -.
                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ranscription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58
88
1112
137
237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S71795; S71795.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
                                                                                                              116 ĠĠ 117
                                                                          50 GG 51
                                                                                                                                                                                                            CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA BIND
                                                                                                                                                                                                              FXGA
                                   셤
                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                             Eukaryota, Viridiplantae, Careptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicoryledons; core endicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                      MEDLINE=97201476; PubMed=9049262; DOI=10.1023/A:1005738910743; Santino C.G., Stanford G.L., Conner T.W.; "Developmental and transgenic analysis of two tomato fruit enhanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.4%; Score 201; DB 2; Length 207; 70.6%; Pred. No. 3.3e-09; tive 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

66.8%; Score 199; DB 2; Length 165;

Best Local Similarity 64.5%; Pred. No. 3.9e-09;

Matches 40; Conservative 0; Mismatches 0; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X95542; CAA64559.1; -.
FIR; T07381; T07381.
HSPP; P24371; HHYP.
InterPro; IPR003612; AAI.
FFfan; PF00234; Tryp_alpha_amyl; 1.
SWART; SM00499; AAI; 1.
SEQUENCE 207 AA; 18265 MW; A50FE71F8ED4C4D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Huttunen S., Vieira J., Hoikkala A.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AY012591, AAG48861.1; -.
Flybase, FBGn0042729; Dvir\nonA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 AA; 15822 MW; FOD87E1E78DCC01F CRC64;
                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No on or off transient A (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                   Lycopersicon esculentum (Tomato).
                                                                                                                                                                                                                                                                                                                                                                                                   Plant Mol. Biol. 33:405-416(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila virilis (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity 70.6%;
36; Conservative
                                                                    01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-SBB;
                                                                                                                                                                                                                                                                                     FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165
                                                                                                                                 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            IISSUE=Fruit;
                                                                                                                                                                                                                                                                                                         TISSUE=Fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Connor T.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=nonA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                   043522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q95UX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
```

à

```
ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDIJINE-20277480; PubMed=10819329;
Nakamura Y.;
"Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
features of the regions of 4,504,864 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                      5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OJUNG: CTENNELLE 15, Created)
01-OCT-2000 (TENNELLE 15, Last sequence update)
01-OCT-2000 (TENNELLE 15, Last sequence update)
Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:K14A17.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicoryledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Gaps
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AB026656; BAA9489.1; -.
SEQUENCE 175 AA; 14340 MW; CC7CD9918498707C CRC64;
                                                                                                              Query Match 66.6%; Score 198.5; DB 1; Length 440; Best Local Similarity 66.1%; Pred. No. 9.7e-09; Matches 37; Conservative 1; Mismatches 13; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 66.4%; Score 198; DB 2; Length 175; Local Similarity 57.6%; Pred. No. 4.9e-09; les 38; Conservative 0; Mismatches 12; Indels
Poly-Pro.
; 82266C2E1E103A48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
    330 P
44669 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clones.";
DNA Res. 7:131-135(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
    321 3
440 AA;
    DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9NST60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
0915NG
AC 0915N AC 0915N DT 01-0C DT 01-0C DT 01-0C DE Arabio OC Sperm OC Sperm (1)
RP SEQUE RY SEQUE
                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
```

Search completed: September 7, 2005, 12:59:57 Job time : 113.5 secs

45 GGGGGG 50 ||| || 104 GGGNGG 109

ò

g

This Page Blank (uspto)

us-09-910-432-20.rag

```
HIV-TAT P
HIW-TAT P
Human GPC
Poly Gly
TZR G-pro
Poly Gly
PINPOINT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rice prot
Chicken m
OsGRP-A1.
Arabidops
Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein e
Streptoco
Protein e
Drosophil
Drosophil
Human gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pro
tra
tra
NF-
                                                                                                                (without alignments)
301.142 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human
                                                                                                ; Search time 65.5 Seconds
                                                                                                                                                                                                  5
                                                                                                                                                                                  Adc65108 Adc85108 Adc86108 Adc87061 Add88556 Add88556 Add86515 Add86715 Add87120 Add871206 Add87159 Add87169 Add87169 Add14649 Add14649 Add14649 Add14649 Add87171 Add8712061 Add87159 Add87169 Add14649 Add14649 Add14649 Add87171 Add87169 Add87169 Add14649 Add14649 Add87171 Add87164 Add87171 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adc65109
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                    of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                   2105692 segs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                              2005, 12:44:44
                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                               protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC65109
ADC65108
ADC65108
ADC65108
ADG8655
ADJ86451
ADJ86649
                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        geneseqp1980s:*
geneseqp290s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:*
geneseqp2003as:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Geneseq 16Dec04:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               geneseqp2004s:*
                                                                                                                                                                                                                                                                                                                                                      length: 0
length: 2000000000
                                                                                                                                                                 US-09-910-432-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
                                                                                                ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    September
                                                                                                                                                                                                                                    BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beq
Beq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298
277
230.5
228.5
228.5
228.5
228.5
228.5
210.5
199.5
199.5
196.5
196.5
196.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192.5
189.5
189.5
189.5
189.5
189.5
                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                  score:
                                                                ı
                                                                                                                                                                                                                                                                                                                   Total number
                                                                                                                                                                                                                                                                                                                                                    Minimum DB
Maximum DB
                                                               protein
                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Result
                                                               Š
```

6 8 ABM81732 Tumour-as 6 8 ADS88302 Ads88302 Human pro 8 4 ABB65751 Abb69751 Drosophil 8 4 ABB65751 Abb65751 Drosophil 2 5 ABG76510 Adm47985 Abg76510 DNA encod 1 6 ABR56404 Abr56404 Peptide l 6 4 AAM78356 Aam78356 Human pro 2 7 ADP08034 Abr41512 Abr41512 Human pro 4 8 AD116318 Ad116318 Human pro	2 AAW41640 Aaw41640 4 AAB86127 Aab86127 7 AD867648 Adb67648 8 ADS88241 Ad688241 4 ABB60364 Abb60364 4 AAW16105 Abb60364 4 AAW18596 Aam16105 4 AAW28596 Aam28599	ALIGNMENTS	entry)		on; follicle; restore; cosmetic; clinical; ical trauma; burn; skin transplant; ulcer;	virus 1.	on/Qualifiers "this region may consist of between 0-20 Gly es" "this region may consist of between 0-20 Gly es"			005564.	ρų.	STEMS INC.		g new hair growth and preventing hair regression on of vascular endothelial growth factor and its a positively charged backbone with attached	7pp; English.	to the induction or stimulation of hair growth.
000004440100	4444666	tandard, peptide	(first ent	tide #2.	regressi kry; surg HIV-TAT.	ic. mmunodeficiency	Locati e 120 /note= residu e 325 /note= residu	9-A2.		; 2003WO-US005564	zus-	ESSENTIA BIOSYSTEMS Dake M;	-845018/78.	or stimulating no administration agonist with a poy	Page 14; 47	relates
26 189.5 22 189.5 29 187. 30 187 31 185.5 33 185.5 34 184.5 35 183.5 183.5 183.5 183.5 183.5 183.5 183.5	1182	RESULT 1 ADC65109 ID ADC65109 8te	ADC65109; 18-DEC-2003	HIV-TAT pept		Synthetic. Human immunc	Misc-differenc Misc-differenc Misc-differenc	WO2003072049	04-SEP-2003	21-FEB-2003	В-2	(ESSE-) ESSI Waugh J, Da	WPI; 2003-84	Inducing or comprises acreceptor aggeticiency	Disclosure;	The invention

pro tra pro

Human Human Human

```
charged backbone having a plurality of attached efficiency groups. The positively charged backbone having a plurality of attached efficiency groups. The positively-charged back bone (preferably polylyaine) comprises a polymer having positively-charged branching groups. The efficiency group is of formula (Gly) n (Arg) m and TAT domains or fragments. The positively-charged backbone has a plurality of efficiency groups of 15000·300000 MW preferably with a polylysine backbone having a plurality of attached Gly 3 Arg 7 groups with 5-30 % degree of lysine saturation. The composition provides stimulation of new hair growth, increase in hair growth or prevention of hair regression by the retention in the number of existing hair follicles roses sectional area, increasing the hair follicle cross-sectional area, increasing the hair follicle cross-sectional area, connected the number of hair follicles and the regrowth of hair follicles. The composition is also useful for restorative purposes and appropriate for use in any situation where there is a need or desire of hair growth such as alopedia, accidental injury, damage to hair follicle, aurgical trauma, burn wound, desire in mammals such as monkeys cats, costs, costs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
endothelial growth factor (VEGF), a VEGF receptor agonist, a prodrug form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dogs, gerbils, gate, guinea pigs, hamsters, horses, mice, prairie dogs, rabbits, rats, sheep's, squirrels and especially humans. The composition can be easily applied and enhances gloss, plow, brilliance, fullness, length, luster, patina, sheen, shine, thickness and volume are improved. (Controlled-release matrix formulation delivers the composition over a 24 (preferably 8) hours period and the matrix is not readily washed off or removed with water. The current sequence represents a HVV-TAT fragment that acts as the positively charged backbone in a composition of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 1. .20
/note= "this region may consist of between 0-20 Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 32. .51
/note= "this region may consist of between 0-20 Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hair; growth; regression; follicle; restore; cosmetic; clinical; alopecia; injury; surgical trauma; burn; skin transplant; ulcer; chemotherapy; HIV-TAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 298; DB 7; 100.0%; Pred. No. 1.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADC65108 standard; peptide; 51 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-FEB-2002; 2002US-0359400P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-2003; 2003WO-US005564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV-TAT peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003072049-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 51 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC65108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 $$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
```

```
The invention relates to the induction or stimulation of hair growth. The method of the invention comprises the administration of vascular endothebial growth factor (VEGF), a VEGF receptor agonist, a produced for endothebial growth factor (VEGF), a VEGF receptor agonist, a produced or its salt form in a non covalent association complex with positively charged backbone having a plurality of attached efficiency groups. The positively-charged backbone have a plurality of efficiency groups of formula (Gly) n (Arg) m and TAI domains or fragments. The positively-charged backbone have a plurality of efficiency groups of 15000-300000 MW preferably with a polylysine backbone having a plurality of attached Gly Groups with 5.30 % degree of lysine saturation. The composition of new hair growth, increase in hair growth or prevention of hair regression by the retention in the number of existing hair follicles. Increasing the hair follicle cross-sectional area, increasing the number of hair follicles and the regrowth of hair follicles. The composition is also useful for restorative purposes of increasing the number of hair follicles and the restorative purposes of appropriate for use in any situation where there is a need or desire of appropriate for use in any situation where there is a need or desire of argical trauma, burn wound, desire to modify physical appearance. Commissional wound, donor site wound from sith transplant, ulcer or radiation of chemotherapy site in mammals such as monkeys cats, cows, dogs, gerbils, gats, guinea pigs, hamsters, horses, mice, prairie dogs, rabbits, rats, sheep's, squirrels and especially humans. The composition can be easily applied and enhances gloss, volusies and volume are improved. Controlled-release matrix formulation delivers the composition over a 24 (preferably 8) hours period and the matrix is not readily washed off or humanium acts as the positively charged backbone in a composition of the current sequence represents a HIV-TAT fragment in a composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                  Inducing or stimulating new hair growth and preventing hair regression comprises administration of vascular endothelial growth factor and its receptor agonist with a positively charged backbone with attached
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    guanosine triphosphate-binding protein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 277; DB 7; Length 51
Pred. No. 1.3e-19;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                            Disclosure; Page 14; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC87061 standard; protein; 920 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human GPCR protein SEQ ID NO:1514.
                    (ESSE-) ESSENTIA BIOSYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 93.0%;
Local Similarity 94.1%;
nes 48; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-2004 (first entry)
                                                                                                       WPI; 2003-845018/78.
                                                                                                                                                                                                                   efficiency groups.
                                                               Dake M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 51 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP1270724-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nvention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC87061;
                                                               Waugh J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADC8706:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
```

ä

Gaps

9 51

Indels

protein

(NAAD-)

```
The invention describes an isolated taste transduction G-protein coupled receptor (I) e.g., T2R which is expressed in a taste cell, comprises greater than 60% sequence identity to a fully defined sequence of 335 (S1), 333 (S2), 299 (S3), 310 (S4), 224 (S5), 77 (S6), 209 (S7), 266 (S8), 300 (S9), 300 (S10), 155 (S11), 173 (S12), 94 (S13), 115 (S14), 68 (S15), 126 (S16) and 180 (S17) amino acids as given in the specification.
                                                                                                                              The present invention relates to a method of identifying a compound that regulates angiogenesis via the modulation of contactin associated protein go (CASPR3). The method involves contacting the compound with a CASPR3 polypeptide and determining the functional effect of the compound upon the CASPR3 polypeptide. The CASPR3 nucleic acid and encoded protein is useful as a drug target for anti-angiogenic therapies. The invention is also useful in gene therapy. The present sequence is poly Gly flexible linker. This sequence is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated taste transduction G-protein coupled receptor e.g., T2R useful for identifying compound that modulates taste signaling in taste
                Methods for identifying compounds which regulate angiogenesis via modulation of contactin associated protein 3 (CASPR3) for the used in diagnosis and therapy of diseases related to angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     taste transduction; G-protein coupled receptor; T2R; taste signaling; cAMP level; cGMP level; IP3 level; Ca(2+) level; electrical activity; human; G-protein coupled receptor; receptor; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.7%; Score 228.5; DB 7; Length 200; 80.4%; Pred. No. 1.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                             12R G-protein coupled receptor related linker seg id 94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mueller
                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 94; 121pp; English.
                                                                                                 Disclosure; SEQ ID NO 14; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ryba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADJ84541 standard; protein; 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hoon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-FEB-2003; 2003US-00364861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00393634
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 80.44
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adler JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-203221/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZUKE/) ZUKER C S. (ADLE/) ADLER J E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUELLER K.
                                                                                                                                                                                                                                                                                                                        Sequence 200 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2004038312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOON M.
RYBA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RYBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ84541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RYBA/)
(MUEL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /NOOH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zuker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADJ84541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ï
                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The protein sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
                                                                                                                                                                                                                                                                                               New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    þe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------666666666666666666666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 7; Length 920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; angiogenesis; contactin associated protein 3; CASPR3;

    .200
    /note= "Gly residues from position 6 to 200 present or absent"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 230.5; DB 7; Length Pred. No. 3.4e-14; 0; Mismatches 1; Indels
                                                                                                                                   NAT INST ADVANCED IND SCI & TECHNOLOGY.
CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
                                                                                                                                                                                                Suwa M, Asai K, Akiyama Y, Aburatani H;
                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; SEQ ID NO 1514; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADG88556 standard; protein; 200 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lorens JB, Xu W, Bogenberger J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 GGGGGGGGGGGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAR-2002; 2002US-00100818.
                                                         18-JUN-2002; 2002EP-00013517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 77.3%;
1 Similarity 80.4%;
41; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAR-2002; 2002US-00100818
                                                                                               18-JUN-2001; 2001JP-00246789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Poly Gly flexible linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RIGE-) RIGEL PHARM INC
                                                                                                                                                                                                                                        WPI; 2003-315783/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-843828/78.
                                                                                                                                                                                                                                                           N-PSDB; ADC87060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 920 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2003176333-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-SEP-2003.
                02-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADG88556;
```

Matches

ઠે 셤 RESULT 4

ADG8855

꿏

```
ä
             in taste cells which involves contacting the compound with (I) and determining the functional effect of the compound (I). The functional effect is a determined by measuring changes in intracellular cAMP, CGMP, IP3, or Ca (2+). The functional effect is a chemical or physical effect. The functional effect is a chemical or physical effect. The functional effect is determined by measuring binding of radiolabeled GTP to (I). (I) is recombinant and is from rat, mouse, or human. (I) is expressed in a cell or cell membrane. The functional effect is measured by determining changes in the electrical activity of cells (e.g., eukaryotic cell) expressing (I). (I) is useful for identifying compound that modulates taste signaling in taste cells which involves contacting a compound with (I). The extracellular domain (II) of (I) is useful for identifying a compound extracellular domain (II) of (I) is useful for identifying a compound
                                                                                                                                                                                                                                     extracellular domain (II) of (I) is useful for identifying a compound that modulates teste signaling in taste cells which involves contacting the compound with the polymuclectide encoding (I) and determining the functional effect of the compound upon the extracellular domain. This is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G-protein coupled receptor 39; GPR 39; cancer; breast; ovary; prostate; brain; lung; ligand binding; aberrant receptor protein analysis; cytostatic; receptor; poly Gly flexible linker.
 useful for identifying a compound that modulates taste signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Residues are independently optionally absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                 amino acid sequence of a T2R G-protein coupled receptor related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>.</u>
و
                                                                                                                                                                                                                                                                                                                                                                                                    / Match 76.7%; Score 228.5; DB 8; Length 200; Local Similarity 80.4%; Pred. No. 1.5e-14; les 41; Conservative 0; Mismatches 1; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADM96215 standard; protein; 200 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-SEP-2002; 2002US-00255775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-2002; 2002US-00255775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Poly Gly flexible linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IMMU-) IMMUSOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 6
                                                                                                                                                                                                                                                                                                                                                                  Sequence 200 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2004071708-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-APR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADM96215;
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
$$$$$$$$$$$$$$$$$$$$$$$$$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
```

The invention relates to a method of identifying anticancer agents that modulate G-protein coupled receptor (GPR) proteins, comprising contacting

Disclosure; SEQ ID NO 3; 33pp; English.

Identifying anticancer agents modulating G-protein coupled receptor proteins, comprises contacting GPR 39-specific binding agents to cand cells and detecting anticancer activity to identify anticancer agent.

Claassen G, Li H, Barber J;

WPI; 2004-373880/35

```
certivity. The invention also relates to a method of inhibiting cancer characteristics in cancer cells by down modilating GRR 39 protein characteristics in cancer cells by down modilating GRR 39 protein cartivity to a level sufficient to inhibit the cancer characteristics of the cancer cells and an antibody that specifically recognises a GPR 39 protein. The method further involves binding a population of different compositions to the GPR 39 protein to select GPR 39-specific binding agents. The cancer cells are chosen from breast, ovarian, prosetate, brain and lung cancer cells. The method is useful for identifying anticancer capture that modulate GPR 39 protein and for inhibiting cancer calls. The method is useful for inhibiting cancer characteristics in cancer cells. The antibody is useful for inhibiting receptor function e.g. by blocking ligand binding, which is used in therapeutic function, in various in vitro histochemical techniques for detecting GPR proteins and as a diagnostic tool for aberrant receptor protein analysis. This sequence represents a poly Gly flexible linker cused in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting whether a first molecule is in close proximity to a second molecule, or detecting target molecule, by using a molecular beacon comprising an oligonucleotide to which a fluorophore and a quencher are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to detecting (M) whether a first molecule is in close proximity to a second molecule, or detecting a target molecule,
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein position identification with nuclease tail; linker; PINPOINT; molecular beacon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  42
                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                               Score 228.5; DB 8; Length 200; Pred. No. 1.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .97
/note= "Optionally absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Optionally absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Col 59-60; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG71303 standard; protein; 201 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PINPOINT poly-Gly linker protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 999999999999999999
                                                                                                                                                                                                                                                                                                                                          76.7%;
80.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0080234P. 97US-00825664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-00054281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-DEC-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 105. .201
                                                                                                                                                                                                                                                                                                                                                                               41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-749290/81.
                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 1
                                                                                                                                                                                                                                                                                                           Sequence 200 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US6444421-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG71303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chung JH;
                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 attached
                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        858888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                 ð
```

```
to which a fluorophore and a quencher (FQ) are attached. The method is named Protein Position Identification with Nuclease Tail (PINPOINT). The method further comprises, whether a first molecule is in close proximity to a second molecule involves attaching a molecular beacon to the first molecule, where the molecular beacon comprises an (ON) to which is attaching an endonuclease (EN) molecy to the second molecule, and determining whether the first molecule is in close proximity to the second molecule by detecting whether fluorescence is emitted by the fluorophore, where fluorescence emission is indicative of cleavage of the (ON) by the (EN) moiety, to cause separation of the (FQ). The method may also comprise, detecting a target molecule, which involves contacting the target molecule with a chimaeric fusion molecule that molecule, thus guiding the chimaeric fusion molecule to the target molecule, contacting the chimaeric endonuclease with a molecular beacon
                                                                                                                                                                                                                                                                                                 comprising an (ON) to which is attached a fluorophore and agencher, and detecting the presence of a fluorescent signal which results from cleavage of the (ON) by the (EN), to allow separation of the quencher from the fluorophore. The method is useful for detecting whether a first molecule is in close proximity to a second molecule, or for detecting a rarget molecule and is useful for detecting interactions in vivo, in situ and in vitro, such as enzymatic reactions, hormoneligand interactions, and drug or toxin interactions. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           yand interactions, and drug or toxin interactions. The present sequence
a proteinlinker used in the PINPOINT constructs of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zyskind JW;
Xu HH;
involves using a molecular beacon that comprises an oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.7%; Score 228.5; DB 5; Length 201; 80.4%; Pred. No. 1.5e-14; ive 0; Mismatches 1; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein encoded by Prokaryotic essential gene #7896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU22369 standard; protein; 188 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001US-00815242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAR-2002; 2002US-0362699P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burkholderia mallei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ACA26239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 201 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU22369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
```

ï

Gapa

screening

New antisense nucleic acids, useful for identifying proteins or scre for homologous nucleic acids required for cellular proliferation to

```
The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the ancienca acid anhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid conciding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated of polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway or required for proliferation, or that that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product or the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the collection of strains; or (13) identifying the target of a compound that inhibits the collection of strains of screening for homologous nucleic acids required for proliferation in calls other than S. aureus, S. typhimurium, C. the target prokaryotic essential genes. Note: The sequence data for this collection, in this direction of the present sequence is encoded by one of the target promate directly from NIPO at collection, but was obtained in electronic format directly from NIPO at encoded by one of the collection of the present sequence is encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----GGGGGGYGRKKRRQRRRGGG----GGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Gaps
isolate candidate molecules for rational drug discovery programs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 214.5; DB 6;
Pred. No. 3.1e-13;
2; Mismatches 6;
                                           Claim 25; SEQ ID NO 50293; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus polypeptide SEQ ID NO 7196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP29010 standard; protein; 56 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-OCT-2001; 2001WO-GB004789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.0%;
67.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 67.2 Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGGGGGGGGGGGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 GGG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200234771-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP29010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP29010
    움
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
ABB64729;
                                    Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB64729
  ઠ
                                                                                                                                                                                                                   The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (31), given in the specification. The proteins have antibacterial and antimiflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. (I) Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detecrain whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1,
                                                                                                                                                 New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                Masignani V, Margarit Y RosI, Grandi G, Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                  chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.6%; Score 210.5; DB 5; Length 56; 74.5%; Pred. No. 2.9e-13; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein encoded by Prokaryotic essential gene #25647.
                                                                                                                                                                                                Claim 1; Page 3875; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU40120 standard; protein; 237 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342921P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
         24-NOV-2000; 2000GB-00028727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 74.5
Hes 38; Conservative
                                                         INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus proteins
                                                                                                                 WPI; 2002-352536/38
                                             CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas putida.
                                                                                                                              N-PSDB; ABN69641
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-OCT-2002.
                                                                               Telford J,
Tettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU40120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                         (GENO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
```

```
the invention relates to an instance in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense another appearance is inhibited by the antisense conclaints a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated contisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting callular contisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting callular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for that has an antibitic cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation for enquired gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent of product is overexpressed or underexpressed; (12) determining the extent of strains; or (13) identifying the target of a compound that inhibits the confound for proliferation of an organism. The antisense nucleic acids are useful for proliferation of an organism. The antisense nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, content required for proliferation in cells other than S. aureus, S. typhimurium, content content did not form part of the printed sequence data for this patent did not form part of the printed specification, but was obtained for proliferation and patent did not form part
                                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid comprising any one of
                                                                                   Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 66.9%; Score 199.5; DB 6; Length 237; Best Local Similarity 70.6%; Pred. No. 1e-11; Matches 36; Conservative 1; Mismatches 5; Indels 9
                                                                                        Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 20979.
                                                                                   Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 25; SEQ ID NO 68044; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB64729 standard; protein; 344 AA
                                                                                   Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
(ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster,
                                                                                   Zamudio C,
Trawick JD,
                                                                                                                                                                                                                         2003-029926/02
                                                                                                                                                                                                                                                                   N-PSDB; ACA43990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-2002
```

ij

```
New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Prosophila. The invention useful in developmental biology and in elucidating cell signalling and cell interactions in higher eukaryotes for the development of
                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                         insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                              Disclosure, SEQ ID NO 6822; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGGGGGG------GGGGGGGGGGGGGGKKRRQRRGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.6%; Score 198.5; DB 4;
67.2%; Pred. No. 1.9e-11;
live 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome derived single exon protein #5655
                      Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABO59421 standard; protein; 208 AA.
                      Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanzel DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-APR-2002; 2002US-00029386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-APR-2002; 2002US-00029386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 67.2
Matches 41, Conservative
                      Adams M,
                                                        WPI; 2001-656860/75.
N-PSDB; ABL04113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PENN S G.
RANK D R.
HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-119264/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             surveying tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2003194704-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 Ġ 270
                                                                                                                                                         interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 G 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2003
                      /enter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABO59421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PENN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HANZ/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (RANK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ë,
                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), processed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 20979; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.8%; Score 199; DB 4; Length 344; 65.1%; Pred. No. 1.5e-11; ive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 6822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGGGGGG----GGGGGGGGGGGGGKKKKRRQRRGGGG-
                                                                                                                                                                                                                Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB60010 standard; protein; 399 AA
                                                                                                                                                                                                                PWD,
                                                                            23-MAR-2001; 2001WO-US009231
                                                                                                               23-MAR-2000; 2000US-0191637P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                ፰
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster
                                                                                                                                                                                                              Venter JC, Adams M,
                                                                                                                                                                                                                                                    WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                         (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                      N-PSDB; ABL08832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGG 70
WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical
                                                                                                                                                                                                                                                                                                                                                   interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002
                                      27-SEP-2001
```

Query Match Best Local S

Matches

49

a Š ABB60010;

RESULT 12 ABB6001

ω ;

17; Gaps

48

18

New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain useful in generating plants having improved

Claim 34; SEQ ID NO 586; 130pp; English.

nutritional properties.

Moughamer T; Ricke D;

Cooper B, Goff SA, Kreps J, Provart N,

Briggs S,

Cheng W, Brigg-

Glazebrook J,

WPI; 2003-229341/22. N-PSDB; ADC08280.

(SYGN ) SYNGENTA PARTICIPATIONS AG

22-JUN-2001; 2001US-0300112P. 26-SEP-2001; 2001US-0325277P. 20-DEC-2001; 2001US-0342327P.

```
The invention relatices to a nucleic acto probe for measuring numan gene expression, comprising any of the 27400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 annino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-defressable set of single exon nucleic acid molecule addressable set of single exon nucleic acid probes for measuring human cells or tissues. Also included are a spatially-deprobes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of exon microarray for measuring human gene expression, a vector comprising at least 8 configuous amino acids of any of the above-mentioned amino acid above, an ORF-encoded peptide comprising at least 8 configuous amino acids of any of the above-mentioned amino acid above, and or special cited above. The probe or microarrays to methods of selling and/or licensing single exon probes or microarrays to subman gene expression data by subscription, and a computer-readable confidence can be expression of a single exon probe cited above. The probes methods and apparatus are useful in percent configured and characterising gross alternative splicing events, in detecting and characterising gross alternative splicing events, in detecting and characterising gross and expressions in the spannic locus that includes their aron, in an analysis of multiple read and included any in principle of any of the supersions. In addition, the probes are used in identifying and characterising of multiple and in any in principle of any of the supersions. In addition, the probes are used in identifying and included any in principle exon, in a suppression and included any of the super
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                           invention relates to a nucleic acid probe for measuring human gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.3%; Score 197.5; DB 8; Length 208; 72.5%; Pred. No. 1.4e-11; ive 0; Mismatches 5; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           segdata.uspto.gov/sequence.html?DocID=20030194704
                             Claim 45; SEQ ID NO 33055; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC08281,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
ઠ
```

plant biotechnology; carbohydrate synthesis; carbohydrate metabolism; carbohydrate degradation; carbohydrate; plant grain; grain filling; corn; tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet; wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain; gene; ds; plant. Gарв 31 dededercedededercederce ----- decedredededercededed 72 , 6 Rice protein sequence Seq ID586 related to grain filling. ADC08281 standard; protein; 162 AA. 

21-JUN-2002; 2002WO-IB002450.

WO2003000905-A2

03-JAN-2003

Oryza sativa

ή,

```
This invention, in the area of plant biotechnology, relates to novel polymucleotides comprising a nuclectide sequence encoding a protein which is involved in or associated with the synthesis, metabolism or degradation of carbobydrates in the plant grain and the expression of which is up regulated during grain filling. The plant is selected from corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco, sugarbeet, wheat, and rice. The invention may be useful for the improvement of protein, oil, starch, fibre and moisture content of the cereal grains. In addition, carbohydrate levels may be modified to a more desirable level using the present invention. The present sequence is the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/publishedpct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rett syndrome; methyl-CpG-binding protein 2; MBCP2; neurodevelopmental disease; autism; non-syndromic mental retardation; idiopathic neonatal encephalopathy; idiopathic infantile spasm; idiopathic cerebral palsy; Angelman syndrome; schizophrenia; chicken.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 decegracecercececes de 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 7; Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.9%; Score 196.5; DB 7; 76.0%; Pred. No. 1.4e-11; 7; wiematches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chicken methyl-CpG-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADK14010 standard; protein; 345 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-SEP-2000; 2000US-00657013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0152778P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 76.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US6709817-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADK14010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADK14010
셤
```

Search completed: September 7, 2005, 12:56:08 Job time : 66.5 secs

This Page Blank (uspto)

```
RESULT 1
US-09-989-981A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 40, Appl
Sequence 22, Appl
Sequence 6, Appli
Sequence 5, Appli
Sequence 112, Appli
Sequence 4, Appli
Sequence 324, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4787, Ap
8322, Ap
7, Appli
7, Appli
57837, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11006, A
4573, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1080, Ap
8319, Ap
9, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12, Appl
4, Appli
3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17, Appl
1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Appl
Sequence 1, Appli
                                                                      September 7, 2005, 12:48:54 ; Search time 29.5 Seconds
    (without alignments)
    129.054 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                  51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1
Sequence 4
Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Sequence S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence Sequence Sequence S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
Sequence
Sequence
                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                         513545
                                                                                                                                                                                                                                                                                                                                                                     1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-989-981A-13
US-09-054-295-1
US-09-054-281-240
US-09-054-281-25
US-09-08-18-094-40
US-09-18-094-40
US-09-18-094-40
US-09-18-094-40
US-09-538-092-1080
US-09-538-092-1080
US-09-538-092-1080
US-09-538-092-1080
US-09-157-349-9
                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               - protein search, using sw model
                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                          Issued_Patents_AA:*
                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                      US-09-910-432-20
298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600.9
600.9
60.9
60.9
7.0
60.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.09
                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              228.5
228.5
228.5
228.5
228.5
228.5
228.5
195.5
195.5
189.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181.5
181.5
181.5
181.5
178.5
178.5
178.5
177.5
176.5
176.5
171.5
                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183
183
                                              OM protein
                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                Sequence:
                                                                                                                                                                                                                Searched:
                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Result
```

```
US-09-98-981A

Sequence 13, Application US/0980981A

Patent No. 682150

GENERAL INFORMATION:

APPLICANT: Balon Barnes, Robert

APPLICANT: Shan Barnes, Robert

APPLICANT: Than Information Tran and Methods of Use

TITLE REFERENCE: 10681 -00732008

TITLE REFERENCE: 10681 -00732008

TITLE REFERENCE: 10681 -00732008

TITLE OF INVENTION -AEGGS and ABGG8: Compositions and Methods of Use

TITLE OF INVENTION -AEGGS and ABGG8: Compositions and Methods of Use

TITLE OF INVENTION -NEGGS and ABGG8: Compositions and Methods of Use

TITLE OF INVENTION -NEGGS and ABGG8: Compositions and Methods of Use

TITLE OF INVENTION -NEGGS and ABGG8: Compositions and Methods of Use

TITLE OF INVENTION -NEGGS and ABGG8: Compositions and Methods of Use

TITLE OF INVENTION -NEGGS and ABGG8: Compositions and Methods of Use

TOWARD APPLICATION WOMER: US 60/252, 235

PRIOR FILLING DATE: 2000-11-20

PRIOR FILLING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 13

SEQ ID NO 13

INVENTION -NEGGS AT APPLICATION -NEGGS AT APPLICANT: Part STATURE: PART STATURE: NEGGS AT APPLICANT: Sivaraja, Mohanzam

PAPILCANT: PAPI
```

ä

```
018781-000800US
                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.43
Matches 41, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: /p

; OTHER INFORMATION: /p

; OTHER INFORMATION: /n

; OTHER INFORMATION: pre

US-09-053-003-40
                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-054-281-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 40, Application US/09053003
; Patent No. 6207391
; GENERAL INFORMATION:
; APPLICANT: Wu, Pengquang
; APPLICANT: Wu, Pengquang
; TITLE OF INVENTION: High-Throughput Screening Assays for
; TITLE OF INVENTION: High-Throughput Screening Assays for
; TITLE OF INVENTION: High-Throughput Screening Assays
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townseend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STAREE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High Throughput In Vitro Screening Assay
for Transcription Modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.7%; Score 228.5; DB 3; Length 201; 80.4%; Pred. No. 2.3e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,995
FLING DATE: 31-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PATENT, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 018781-000600US
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/09/053,003 FILING DATE: 31-MAR-1998 CLASSIFICATION: 435
                                        NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Twomsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                               ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111-3834
COMPUTER REALABLE FORM:
CMDIUM TYPE: Floppy disk
CMDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 576-0300
INPORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 201 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-09-053-003-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-052-995-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                      9;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/09054281
Fatent No. 644421
GENERAL INFORMATION:
APPLICANT: Chung, Jay H.
TITLE OF INVENTION: Methods for Detecting Intermolecular TITLE OF INVENTION: Interactions In Vivo and In Vitro
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
FTREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA.
                                                                                                                                                                                                                                                                                                                                       76.7%; Score 228.5; DB 3; Length 201; 80.4%; Pred. No. 2.3e-15; ive 0; Mismatches 1; Indels 9
                                                                                                                                                                                                     /product= "OTHER"
/note= "Gly at positions 105-201 may
present or absent"
                                                                                /note= "Gly at positions 1-97 may be present or absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT PAPLICATION DATA:

APPLICATION NUMBER: US 60/054,281

FILING DATE: 02-APR-1998

CLASSIFICATION NUMBER: US 60/080,234

FILING DATE: 03-APR-1997

PRIOR APPLICATION NUMBER: US 60/080,234

FILING DATE: 03-APR-1997

APPLICATION NUMBER: US 60/080,234

FILING DATE: 03-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Smith, Timothy L.

REFERENCE/POCKET NUMBER: 35,367

REFERENCE/POCKET NUMBER: 35,367

TELEPHONE: (415) 576-0300

TELEPHONE: (415) 576-0300

INFORMATION FOR SEQ ID NO: 22:
OTHER INFORMATION: /product= "OTHER" OTHER INFORMATION: /note= "Gly at pos OTHER INFORMATION: present -- FRATURE:
```

ij

```
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Shan, Bei
APPLICANT: Okamoto, Arthur Y.
APPLICANT: Okamoto, Arthur Y.
APPLICANT: Olarik Inc.
ITILE OF INVENTION: Metabolism
TITLE OF INVENTION: Metabolism
TITLE OF INVENTION: Metabolism
FILE REFERENCE: 018781-001310US
CURRENT APPLICATION NUMBER: US/09/478,948
CURRENT FILING DATE: 1999-01-06
PRIOR APPLICATION NUMBER: US 60/115,249
PRIOR APPLICATION NUMBER: US 60/115,249
PRIOR APPLICATION NUMBER: US 60/115,249
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENTH: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence:flexible linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: MOD RES
; LOCATION: (105)..(201)
; OTHER INFORMATION: Gly at positions 105-201 may be present or absent US-09-478-948-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 105..201
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Gly at positions 105-201 may be OTHER INFORMATION: present or absent"
                                                                                                                                                                                                                                                                                                                                                                                                                        ch 76.7%; Score 228.5; DB 4; Length 201; 1 Similarity 80.4%; Pred. No. 2.3e-15; 41; Conservative 0; Mismatches 1; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 201;
                                                                                             OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Gly at positions 1-97 may be OTHER INFORMATION: present or absent"
NAME/KEY: Modified-site
LOCATION: 105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 76.7%; Score 228.5; DB 4; Length ;
1 Similarity 80.4%; Pred. No. 2.3e-15;
41; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1). (97)
OTHER INFORMATION: Gly at positions 1-97 may be present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 40, Application US/09818094
; Patent No. 6682898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-478-948-6; Sequence 6, Application US/09478948; Patent No. 6465288; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                   LENGTH: 201 amino acids
TYPE: amino acid
STRANDEDNESS:
SEQUENCE CHARACTERISTICS
                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 41; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 41; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MOD_RES
LOCATION: (1)..(9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-818-094-40
                                                                                                                                                                                                                                                                                                                                                                                US-09-054-281-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wu, Pengguang
APPLICANT: Wu, Pengguang
MCKinney, Judi
TITLE OF INVENTION: High-Throughput Screening Assays for
Modulators of STAT4 and STAT6 Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.7%; Score 228.5; DB 4; Length 201; 80.4%; Pred. No. 2.3e-15; tive 0; Mismatches 1; Indels 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09754947
Sequence 5, Application US/09754947
Betent No. 6828110
GENERAL INFORMATION:
APPLICANT: Lee, Bruce Andrew
APPLICANT: Flores, Becky Mar
APPLICANT: Walkirs, Gunars Edwin
APPLICANT: Blosite Diagnostics, Inc.
TITLE OF INVENTION: Assays for Detection of Bacillus Anthracis
                                                                                                                                                                                      CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REPERENCE/DOCKET NUMBER: 31,367
RELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFARA: (415) 576-0300
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Gly at positions 105-201 may be present or absent" SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/053,003
FILING DATE: 31-WAR-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/818,094
FILING DATE: 26-Mar-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..97
OTHER INFORMATION: /product=
/note= "Gly at positions 1-97
present or absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Modified-site
LOCATION: 105.201
OTHER INFORMATION: /proc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 201 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 80.4
Matches 41, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-818-094-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
US-09-754-947-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
```

```
APPLICANT: Kaser, Matthew R.

TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REPERBRY
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REPERBRY
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT PILING DATE: 2002-09-09
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 34
LENGTH: 462
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 dededesegededesegedesegedededesegene----rregenededegededededed 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GGGGGGGGGGRKKRRQRRRGGGGGGGGGGGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-538-092-1080
US-09-538-092-1080
Sequence 1080, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Glot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same;
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.6%; Score 192.5; DB 4; Length 462; 48.2%; Pred. No. 1.3e-11; ive 3; Mismatches 6; Indels 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 162;
; Sequence 4, Application US/09575574;
; Patent No. 6376750;
; GENERAL INFORMATION:
; APPLICANT: Yu. St.-May;
; APPLICANT: Chao, Yu-Chan;
; TITLE OF INVENTION: PLANT SEEDLING AND EMBRYO PROMOTER;
; FILE REPERENCE: 08919-047001;
; CURRENT APPLICATION NUMBER: US/09/575,574;
; CURRENT FILING DATE: 2000-05-22;
NUMBER OF SEQ ID NOS: 10;
; SOFTWARE: FASELSEQ for Windows Version 4.0;
; SEQ ID NO 4;
; LENGTH: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 1813444CD1
US-09-919-039-324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 194; DB 3, Pred. No. 4e-12; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 GGGGGYNRSSGGYEPRGRGGGRGG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 GGGGG------GGGGGG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 324, Application US/09919039
Patent No. 6727066
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.1%;
65.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 65.0
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 48.2
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-575-574-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-09-919-039-324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 112, Application US/09657013

Retent No. 6709817

GENERAL INFORMATION:
APPLICANT: Soghbl, Huda Y.
APPLICANT: Van den Veyver, Ignatia B
APPLICANT: Van den Veyver, Ignatia B
APPLICANT: Amir, Ruthie
APPLICANT: Amir, Ruthie
APPLICANT: Prancke, Uta
TITLE OF INVENTION: Methods of Identifying Mutations in a Methyl-CPG-Binding Domain
TITLE OF INVENTION: Containing Gene or Protein in Neurodevelopmental Disease and Tre
FILE REPERENCE: HO-P01893UG1/09905371
CURRENT FILING DATE: 2000-09-07

PRIOR APPLICATION NUMBER: US 60/152,778

PRIOR FILING DATE: 1999-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 -----KKRRQRRRGGGGGGGGG 44
                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence:flexible linker NAME/KEY: MOD RES

LOCATION: (1)-(97)

OTHER INFORMATION: G17

NAME/KEY: MOD RES

LOCATION: (105)..(201)

LOCATION: (105)..(201)

CORPATION: (105)..(201)

CORPATION: G17 at positions 105-201 may be present or absent used to severe the control of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.7%; Score 228.5; DB 4; Length 201; 80.4%; Pred. No. 2.3e-15; tive 0; Mismatches 1; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.4%; Score 195; DB 4; Length 345; 34.6%; Pred. No. 6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 6e-12;
2; Mismatches
                                  CURRENT APPLICATION NUMBER: US/09/754,947
CURRENT FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: US 60/174,901
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PARENTIN Ver. 2.1
SEQ ID NO 5
LENGTH: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGGGGGGGGGGG--GGGGYGR--
          FILE REFERENCE: 014907-003310US
                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity 80.4%;
41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 41, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 44; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 ĠĠĠĠVĠĠ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGGGG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -09-657-013-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-657-013-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
US-09-575-574-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45
```

요 ò 엄 ઠ

ò

ò g

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 eccececececicis de la constant de la constant de constant de constant de la co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INPORMATION:
APPLICANT: SHINTANI, Yasushi
APPLICANT: SHINTANI, Yasushi
APPLICANT: KANAMOTO, Tomohiro
ITILE OF INVENTION: NOVEL PROTEINS, THEIR PRODUCTION
ITILE OF INVENTION: AND USE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.4%; Score 183; DB 2;
73.9%; Pred. No. 6.9e-11;
tive 0; Mismatches 12;
                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,099A
FILING DATE: 04-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 083649/1996
FILING DATE: 05-APR-1996
APPLICATION NUMBER: 97105508.2
FILING DATE: 03-APR-1997
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATURG SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/157,349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/835,099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/09157349
Patent No. 6068990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Resnick, David S
REGISTRATION NUMBER: 34,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 47:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 268 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 61.4
Best Local Similarity 73.9
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS LENGTH: 268 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-08-835-099A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02109
                                                                          02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-09-157-349-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8319, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 8319
LENGTH: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 GGGGGGGGGNYGQDQSSMSSGGGSGGGYGNQDQSGGGGSGGYGQQDRGGRGGRGGSGGGG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------GGG-----GGGGGGGGGGGRKKRRQRRRGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGGYGRKKRRQRRRGGGGGGGGGGGGGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----RGGRGEGGGRGGGGGGGRG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.6%; Score 183.5; DB 4; Length 112; 69.2%; Pred. No. 3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.6%; Score 189.5; DB 4; Length E
48.2%; Pred. No. 2.9e-11;
tive 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/08835099A
Fatent No. 5874277
GENERAL INFORMATION:
APPLICANT: SHINTANI, Yasushi
APPLICANT: KAWAMOTO, TOMONING
TITLE OF INVENTION: NOVEL PROTEINS, THEIR PRODUCTION
TITLE OF INVENTION: AND USE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (0)...(0)
CTHER INFORMATION: Polypeptide Accession Number P35637
US-09-538-092-1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR PILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 1080
LENGTH: 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 GGGGGGYNRSSGGYEPRGRGGGRGG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GGGGGG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- GGGGGGGGGGGGGKKGGGGW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGGGGGGGGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 48.2
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 69.2
nes 36; Conservative
                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 GGGGGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-09-543-681A-8319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-543-681A-8319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-835-099A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
```

셤

셤 8

ò

```
RESULT 15
US-09-832-297A-12
i Sequence 12, Application US/09832297A
i Patent No. 6652836
i GENERAL INFORMATION:
i APPLICANT: Fluorobrobe, Inc.
i APPLICANT: LUIKEN, George A.
i TITLE OF INVENTION: METHOD FOR VIEWING TUMOR TISSUE LOCATED WITHIN A BODY CAVITY:
I TITLE OF INVENTION NUMBER: US/09/832,297A
CURRENT RPLING DATE: 1299-07-28
PRIOR APPLICATION NUMBER: US/09/32,297A
CURRENT FILING DATE: 1999-10-16
PRIOR APPLICATION NUMBER: US/09/32,190
PRIOR PILING DATE: 1998-10-15
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (3)...(57)

COTHER INFORMATION: Amino Acids at residues 3 to 7 could be repeated up to 10 times US-09-832-297A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:

MARKEY: REPEAT

LOCATION: (3)..(6)

OTHER INFORMATION: Amino Acid at residue 3 could be repeated up to 3 times
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 60.9%; Score 181.5; DB 4; Length 60; Best Local Similarity 66.0%; Pred. No. 2.8e-11; Matches 33; Conservative 0; Mismatches 8; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 61.4%; Score 183; DB 3; Length 268; Best Local Similarity 73.9%; Pred. No. 6.9e-11; Matches 34; Conservative 0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 dedececececicos de como de consecuencia de consecuencia en consecuencia de 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: September 7, 2005, 13:01:57 Job time: 29.5 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Peptide linker moiety
APPLICATION NUMBER: 97105508.2
FILING DATE: 03-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: RESTATION:
NAME: RESTATION: 34,235
REFERENCE/DOCKET NUMBER: 47342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELERAX: 617-523-6440
TELERAX: 617-523-6440
TELERAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: Amino acid
STRANDEDNESS: single
TYPE: MOLECULE TYPE: protein
US-09-157-349-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 윰
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
September 7, 2005, 12:54:00; Search time 57 Seconds (without alignments) 352.368 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                51
                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1774312 segs, 393823214 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                     US-09-910-432-20
298
                                   Copyright
                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                    Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES		
Result No.	Score	% Query Match	% Query Match Length DB ID	DB	ID	Description	
1	298	100.0	51	10	US-09-910-432-20	Sequence 20, Appl	
8	277	93.0		10	US-09-910-432-19	Sequence 19, Appl	
m	230.5	77.3		15	US-10-292-798-1514	Sequence 1514, Ap	
4	228.5	76.7		δ	US-09-798-584-18	Sequence 18, Appl	
5	228.5	76.7	200	σ	US-09-967-624-19	Sequence 19, Appl	
9	228.5	76.7		σ	US-09-998-667-18	Sequence 18, Appl	
7	228.5	76.7		10	US-09-921-159-34	Sequence 34, Appl	
æ	228.5	76.7		10	US-09-990-940-21	Sequence 21, Appl	
6	228.5	76.7		10	US-09-989-981A-13	Sequence 13, Appl	
10	228.5	76.7		10	US-09-850-948-29	Sequence 29, Appl	
11	228.5	76.7		14	US-10-160-354-4	Sequence 4, Appli	

21,	Sequence 3, Appli Sequence 3, Appli	15,	25,	13,	53	ທັ	m	'n	Н	ĩ	'n	12	4, 7	2	23	'n	5	٠.,	٠,	Sequence 521, App	٠.,	• •	•	,	78	6	7,	32,	72,	96,	10,
US-10-026-331B-21 US-10-026-021-8	US-10-161-165-3 US-10-160-663-3	10-01	10-094-417-2	10-188-405-1	US-10-273-575-29	US-10-233-098-5	10-245-850-	US-10-293-582-27	US-10-100-818-14		US-10-321-204-54		US-10-123-568-4	_	1	10-352-724-	US-10-328-916-57	US-10-452-015-3		10-231	10-	10-	US-10-339-744-4	-	US-10-620-052A-78	US-10-794-897-9	US-10-616-403-7	10-679-102-	10-696-909A-7	10-491-54	US-10-805-075-10
14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	15	15	15	15	15	15	12	12	12	16	16	16	11	17	11	18	18
200	200	200	200	200	200	200	200	200	200	200	200	200	200	200	200	200	200	200	200	200	200	200	200	200	200	200	200	200	200	200	200
76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7
228.5	228.5 228.5		-:		228.5			228.5	228.5	228.5	228.5	228.5	228.5	228.5	228.5	228.5	228.5	228.5	228.5	228.5	228.5	228.5	228.5	228.5					228.5		228.5
113	14 15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
Sequence 20, Application US/09910432
Sequence 20, Application US/09910432
Sequence 20, Application US/09910432
Sequence 20, Application No. US20030229034A1
GENERAL INFORMATION:
APPLICANT: Waugh, Jacob
APPLICANT: Essentia Biosystems, Inc.
TITLE OF INVENTION: Multi-Component Biological Transport Systems
FILE REFERENCE: 020154-000110US
CURRENT FILING DATE: 2000-07-20
PRIOR PILING DATE: 2000-07-21
PRIOR PILING DATE: 2000-07-21
SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Charged HIV-TAT fragment branching group
OTHER INFORMATION: (efficiency group) attached to solid backbone
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1) -. (20)
CTHER INFORMATION: (3) at positions 1-20 may be present or absent
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (3) -. (51)
CTHER INFORMATION: (3) at positions 32-51 may be present or absent
US-09-910-432-20
```

셤

```
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (302)..(303)
OTHER INFORMATION: Variable amino acid
                                                               NAME/KEY: MOD RES
LOCATION: (119)..(166)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MOD RES
LOCATION: (233)..(233)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MOD RES
LOCATION: (321)..(321)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (429)...(429)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (434)...(434)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                      LOCATION: (169)...(186)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                FEATURE:
NAME/KEY: MOD_RES
LOCATION: (188)...(188)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                          LOCATION: (215)..(215)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MOD RES
LOCATION: (231)..(231)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (289)...(289)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (295)..(295)

OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (316)..(316)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (345)..(345)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (354)..(354)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (265)..(265)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (350)...(350)
OTHER INFORMATION: Variable amino acid
                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: MOD_RES
LOCATION: (467)..(467)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MOD_RES
COCATION: (289)..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MOD RES
LOCATION: (354)..
                                                                                                                                                       NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                         NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: P
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                   RESULT 2
US-09-910-432-19
is Sequence 19, Application US/09910432
is Sequence 19. Application US/09910432
is Publication No. US20030229034A1
is GENERAL INFORMATION:
is APPLICANT: Waugh, Jacob
is APPLICANT: Essentia Biosystems, Inc.
is TITLE OF INVENTION: Multi-Component Biological Transport Systems
if TITLE OF INVENTION: Multi-Component Biological Transport Systems
is TITLE OF INVENTION: Multi-Component Biological Transport Systems
is TITLE APPLICATION NUMBER: US/09/910,432
is CURRENT FILING DATE: 2001-07-20
is PRIOR FILING DATE: 2000-07-21
is NUMBER OF SEQ ID NOS: 20
is SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEATURE:
NAME/KEY: MOD RES
LOCATION: (32)...(51)
OTHER INFORMATION: Gly at positions 32-51 may be present or absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEATURE:
MAME/KEX: MOD RES
LOCATION: (1) .. (20)
OTHER INFORMATION: Gly at positions 1-20 may be present or absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRATURE:
OTHER INFORMATION: Description of Artificial Sequence:positively
OTHER INFORMATION: charged HIV-TAT fragment branching group
OTHER INFORMATION: (efficiency group) attached to solid backbone
                                                                                     ö
Query Match
Best Local Similarity 100.0%; Pred. No. 9.8e-18;
Matches 51; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 93.0%; Score 277; DB 10; Length 51; Best Local Similarity 94.1%; Pred. No. 5e-16; Matches 48; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 19
LENGTH: 51
TYPE: PRE
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-292-798-1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-910-432-19
```

ò 유

```
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (479)...(479)
OTHER_INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MOD RES
COCATION: (556)..(603)
JTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WANE/KEY: MOD RES
LOCATION: (633)..(633)
JTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MOD RES
LOCATION: (642)..(642)
JTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAWE/KEY: MOD RES
LOCATION: (645)...(645)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MOD RES
LOCATION: (651)..(651)
JTHER INPORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MOD RES
LOCATION: (671)..(671)
JTHER INFORMATION: Variable amino acid
                                           NAME/KEY: MOD RES
LOCATION: (469)...(469)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                     LOCATION: (485)...(485)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                        NAME/KEY: MOD RES
LOCATION: (492)...(492)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MOD RES
COCATION: (551)..(551)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MOD RES
OCATION: (607)..(622)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCATION: (624).. (625)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MOD RES
OCATION: (631)..(631)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: MOD RES
LOCATION: (636)..(636)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (655).. (656)
OTHER INFORMATION: Variable amino acid
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                         COCATION: (499). (499)

THER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (664)..(664)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                          FEATURE:
NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                    IAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MOD RES
```

```
RESULT 4

US-09-798-584-18

i Sequence 18, Application US/09798584

patent No. US2002010267641

GENERAL INFORMATION:
APPLICANT: Mu. David
APPLICANT: Tularik Inc.
TITLE OF INVENTION: KCNB: A No. US20020102676A1e1 Potassium Channel Protein
FILE REFERENCE: 018781-004010US
CURRENT APPLICATION NUMBER: US/09/798,584
CURRENT FILING DATE: 2001-03-03
PRIOR APPLICATION NUMBER: US 60/186,951
PRIOR FILING. DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN OF SEQ ID NOS: 18
SOFTWARE: PATENTIN OF SEQ ID NOS: 18
SOFTWARE: PATENTIN OF SECTIPATION OF ARTIFICIAL SEQUENCE
FRATURE:
COTHER INFORMATION: Description of Artificial Sequence
FRATURE:
COTHER INFORMATION: Gly at positions 6-200 may be present or absent
US-09-798-584-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 15; Length 920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 77.3%; Score 230.5; DB 15; Length Best Local Similarity 80.4%; Pred. No. 2.3e-11; Matches 41; Conservative 0; Mismatches 1; Indels
NAME/KEY: MOD RES
LOCATION: (676)..(676)
OTHER INFORMATION: Variable amino acid
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: MOD_RES
LOCATION: (731)..(731)
OTHER INFORWATION: Variable amino acid
                                                                                                                                                                                                   LOCATION: (683)...(684)
OTHER INFORMATION: Variable amino acid
FEATURE:
                                                                                                                                                                                                                                                                         NAME/KEY: MOD RES
LOCATION: (698)...(699)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                          NAMEKEY: MOD RES
LOCATION: (715)..(715)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: MOD RES
LOCATION: (723)..(723)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEX: MOD RES
LOCATION: (725)..(726)
OTHER INFORMATION: Variable amino acid
                                                                                      NAMELYKEY: MOD RES
LOCATION: (678)..(678)
OTHER INFORMATION: Variable amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MOD RES
LOCATION: (73\overline{6})..(736)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

76.7%; Score 228.5; DB 9; Length 200;

Query Match

7

Gaps

6

Length 200; Indels

셤

ઠે

```
APPLICANT: Jegla, Timothy James
APPLICANT: Witzel, Julie Dickson
APPLICANT: Mitzel, Julie Dickson
APPLICANT: ICAGE, Inc.
TITLE OF INVENTION: Slo2 and Slo4, Novel Potassium Channel Proteins from
TITLE OF INVENTION: Human Brain
FILE REFERENCE: 018512-006810US
CURRENT FILING DATE: 2002-01-17
PRIOR APPLICATION NUMBER: US 60/249,112
PRIOR FILING DATE: 2000-11-15
PRIOR FILING DATE: 2000-11-15
                           FEATURE:
OTHEN INFORMATION: Description of Artificial Sequence:flexible linker:
OTHEN INFORMATION: Description of Artificial Sequence:flexible linker:
NAME/KEY: MOD RES
LOCATION: (6) - (200)
OTHEN INFORMATION: Gly at positions 6-200 may be present or absent US-09-998-667-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence:poly Gly OTHER INFORMATION: flexible linker NAME/KEY: MOD RES LOCATION: (6)...(200)

COTHER INFORMATION: Gly at positions 6-200 may be present or absent US-09-921-159-34
                                                                                                                                                                                                                                                                                                                 Query Match 76.7%; Score 228.5; DB 10; Length 200; Best Local Similarity 80.4%; Pred. No. 1.1e-11; Matches 41; Conservative 0; Mismatches 1; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: An, Songzhu
APPLICANT: Dai, Kang
APPLICANT: Dai, Kang
APPLICANT: Tularik Inc.
TITLE OF INVENTION: No. US20030027252A1el Receptors
FILE REFERENCE: 018781-007410US
                                                                                                                                                                                                                        DB 9;
                                                                                                                                                                                                                      Query Match 76.7%; Score 228.5; DB 9; Best Local Similarity 80.4%; Pred. No. 1.1e-11; Matches 41; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/990,940 CURRENT FILING DATE: 2001-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-921-159-34
. Sequence 34, Application US/09921159
. Publication No. US20030017533A1
. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/09990940 Publication No. US20030027252A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 34
LENGTH: 200
TYPE: PRT
ORGANISM: Artificial Sequence
    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao, Jiagang
Chen, Jin-Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cutler, Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tian, Hui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-09-990-940-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ï
                                  ij
                                  9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (6). (200)
OTHER INFORMATION: Gly residues from position 6 to 200 may be present
OTHER INFORMATION: or absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...aoran
...uu, Peter
...urf: Pardo, Jorge
...rFLICANT: Rigel Plarmaceuticals, Incorporated
..rFLICANT: Rigel Plarmaceuticals, Incorporated
.TITLE OF INVENTION: TRACI: Modulators of Lymphocyte Activation
.TITLE OF INVENTION: TRACI: Modulators of Lymphocyte Activation
.FILE OF INVENTION NUMBER: US 00/998,667
.CURRENT FILING DATE: 2001-12-03
.PRIOR PILING DATE: 2001-04-06
.NUMBER OF SEQ ID NOS: 18
.SQFTWARE: Patentin Ver. 2.1
.SQT ID NO 18
.LENGTH: 200
.TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence:poly Gly tag
OTHER INFORMATION: flexible linker
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Pardo, Jorge
APPLICANT: Pardo, Jorge
APPLICANT: Li, Congfen
APPLICANT: Tabo, Hacran
APPLICANT: Wi, Jun
APPLICANT: Rigel Pharmaceuticals, Inc.
TITLE OF INVENTION: PAK2: Modulators of Lymphocyte Activation
FILE REFERENCE: 021044-00070009
CURRENT APPLICATION NUMBER: US/09/967,624
CURRENT APPLICATION NUMBER: US 60/280,647
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 200
                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.7%; Score 228.5; DB 9; Length 200; 80.4%; Pred. No. 1.1e-11;
                                                                            80.4%; Pred. No. 1.1e-11; trive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                    Sequence 19, Application US/09967624
Patent No. US20020142325A1
GENERAL INFORMATION:
APPLICANT: Liao, X. Charlene
APPLICANT: Chu, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
Best Local Similarity 80.45 Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 80.4 Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: MOD RES
                                                                                                                                                                                             RESULT 5
US-09-967-624-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-09-998-667-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-967-624-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
```

ä

Gaps

٠. د

셤

ð

```
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 4
LENGTH: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-10-160-354-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Shan, Bell APPLICANT: Shan, Bell APPLICANT: Shan, Bell APPLICANT: Tian, Hui APPLICANT: Board of Regents, The University of Texas System TITLE OF INVENTION: ABCGS and ABCG8: Compositions and Methods of Use TIER REFERENCE: 018781-007320US CURRENT APPLICATION NUMBER: US/09/989, 981A CURRENT PILING DATE: 2002-07-23 FRIOR PILING DATE: 2000-11-20 FRIOR PLLING DATE: 2000-11-20 FRIOR PILING DATE: 2000-11-28 FRIOR PILING DATE: 2000-11-28 FRIOR FILING DATE: 2000-11-28 FRIOR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence:flexible linker NAME/EX: NOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence:flexible linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) LOCATION: (6)...(200)
; OTHER INFORMATION: Gly at positions 6-200 may be present or absent
US-09-989-981A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (6)...(200); OTHER INFORMATION: Gly at positions 6-200 may be present or absent US-09-990-940-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.7%; Score 228.5; DB 10; Length 200; 80.4%; Pred. No. 1.1e-11; Live 0; Mismatches 1; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.7%; Score 228.5; DB 10; Length 200; 80.4%; Pred. No. 1.1e-11; Live 0; Mismatches 1; Indels 9;
PRIOR APPLICATION NUMBER: US 60/252,841
PRIOR FILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-12-22
PRIOR PRIOR DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-11-12
PRIOR PLING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 54
SOPTWARE: PALENTIN VEY: 2.1
SOPTWARE: PALENTIN VEY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 13, Application US/0998991A; Publication No. US20030049730A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hobbs, Helen H. APPLICANT: Shan, Bei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 41; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-989-981A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 13
LENGTH: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
```

```
Sequence 4, Application US/10160354

Publication No. US20030013107A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Clu, Peter
APPLICANT: Li, Congfen
APPLICANT: Liao, X. Charlene
APPLICANT: Liao, X. Charlene
APPLICANT: Liao, X. Charlene
APPLICANT: Algel Pharmaceuticals, Incorporated
TITLE OF INVENTION: Alpha 2 Intergrin: Modulators of Lymphocyte Activation
FILE REFERENCE: 201044-001100S
CURRENT APPLICATION NUMBER: US/10/160,354
CURRENT FILING DATE: 2002-05-30
FRIOR PEPLICATION NUMBER: US 60/296,819
PRIOR FILING DATE: 2001-06-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ı;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                    APPLICANT: Yang, Jianxin
APPLICANT: Yan, Songabu
APPLICANT: Thlarik Inc.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Associated With Cancer
TITLE OF INVENTION: Polypeptides and Nucleic Acids Associated With Cancer
FILE REPERENCE: 018781-008300US
CURRENT APPLICATION NUMBER: US/09/850,948
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 29
LENGTH: 200
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence:flexible linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MOD_RES

1 LOCATION: (6)..(200)

2 OTHER INFORMATION: Gly at positions 6-200 may be present or absent

US-10-160-354-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: MOD RES
LOCATION: (6)...(200)
COTHER INFORMATION: Gly at positions 6-200 may be present or absent US-09-850-948-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 76.7%; Score 228.5; DB 10; Length 200; Best Local Similarity 80.4%; Pred. No. 1.1e-11; Matches 41; Conservative 0; Mismatches 1; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 76.7%; Score 228.5; DB 14; Length 200; Best Local Similarity 80.4%; Pred. No. 1.1e-11; Matches 41; Conservative 0; Mismatches 1; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence:poly-Gly OTHER INFORMATION: flexible linker
Sequence 29, Application US/09850948
Publication No. US20030059770A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
```

```
Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MOD_RES

LOCATION: (6) - (200)

LOCATION: (6) - (200)

OTHER INFORMATION: Gly residues from position 6 to 200 may be present

OTHER INFORMATION: or absent
US-10-026-3318-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/10026021

Publication No. US20030027756A1

FURDIAL INFORMATION:

APPLICANT: Hitcosh, Yasumichi
APPLICANT: Demo, Susan

APPLICANT: Menchins, Yonchu

APPLICANT: Rigel Pharmaceuticals, Inc.

TITLE OF INVENTION: Treatment of Callular Proliferation for TITLE OF INVENTION: Treatment of Cancer

TITLE OF INVENTION: USAK: Modulation of Cellular Proliferation for TITLE OF INVENTION: USAK: Modulation of Cellular Proliferation for TITLE OF INVENTION: UNMBER: US/10/026,021

CURRENT APPLICATION NUMBER: US 60/309,632

FRIOR PEDLICATION NUMBER: US 60/309,632

FRIOR PEDLING DATE: 2001-08-01

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:flexible linker
                                                                                                                                                                                                  Sequence 21. Application US/10026331B
Fublication No. US20030027167A1
GENERAL INFORMATION:
APPLICANT: Hitoshi, Yasumichi
APPLICANT: Hitoshi, Yasumichi
APPLICANT: Demo, Susan
APPLICANT: Jenkins, Yonchu
APPLICANT: Jenkins, Jenkins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / LOCATION: (6)...(200)
// OTHER INFORMATION: Gly at positions 6-200 may be present or absent US-10-026-021-8
9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 76.7%; Score 228.5; DB 14; Length 200; Best Local Similarity 80.4%; Pred. No. 1.1e-11; Matches 41; Conservative 0; Mismatches 1; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence:poly Gly
OTHER INFORMATION: flexible linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MOD RES
LOCATION: (6)..(2)
                                                                                                                                                                                        US-10-026-331B-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 8
LENGTH: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
```

```
ä
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEATURE:
NAME/KEY: MOD RES
LOCATION: (6)_.(200)
OTHER INFORMATION: Gly residues from position 6 to 200 may be present
OTHER INFORMATION: or absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Relain, Sacha
APPLICANT: Relain, Sacha
APPLICANT: Rolain, Alex
APPLICANT: Royal Pharmaceuticals, Incorporated
TITLE OF INVENTION: CD43: Modulators of Mast Cell Degranulation
FILE REFERENCE: 021044-001010US
CURRENT FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: US 60/296,801
PRIOR PLING DATE: 2001-06-07
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/10160663

Fublication No. US20030040001A1

GENERAL INFORMATION:

APPLICANT: Demo, Sugan

APPLICANT: Hitoshi, Yasumichi

APPLICANT: Pearsall, Denise

TITLE OF INVENTION: LETMI: Modulators of Cellular Proliferation

FILE REFERENCE: 021044-000920US

CURRENT APPLICATION UNDERR: US 60/296,817

FRIOR APPLICATION NUMBER: US 60/296,817

PRIOR APPLICATION NUMBER: US 60/347,970

FRIOR FILING DATE: 2001-06-07

PRIOR FILING DATE: 2001-06-07

PRIOR FILING DATE: 2001-06-07

PRIOR FILING DATE: 2001-06-07

PRIOR FILING DATE: 2001-06-07

FRIOR FILING DATE: 2001-06-07

FRIOR APPLICATION NUMBER: US 60/347,970

FRIOR FILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 3

LENGTH: 200
                                                                                                                                                                   1 decededecedecedecedeces -----decedecedecedecedes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----- GGGGGGGGGGGGGGGGGGG 42
                                                           6
                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 228.5; DB 14; Length 200;
Pred. No. 1.1e-11;
0; Mismatches 1; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 76.7%; Score 228.5; DB 14; Length 200; Best Local Similarity 80.4%; Pred. No. 1.1e-11; Matches 41; Conservative 0; Mismatches 1; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:poly Gly
OTHER INFORMATION: flexible linker
                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/10161165
Publication No. US20030027763A1
GENERAL INFORMATION:
APPLICANT: Bennett, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 66666666666666666666666
ch 76.7%;
1 Similarity 80.4%;
41; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
```

Search completed: September 7, 2005, 13:03:57 Job time: 57 secs

g

This Page Blank (uspto)

```
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

OM protein - protein search, using sw model

September 7, 2005, 12:47:59 Run on:

9; Search time 24 Seconds (without alignments) 204.461 Million cell updates/sec

US-09-910-432-20 Title: Perfect score:

Sequence:

51

**BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description			RNA-binding protei	glycine-rich RNA-b	hypothetical prote	glycine-rich prote			hypothetical prote			glycine-rich prote	_			_			glycine-rich RNA-b	FUS/CHOP mutant fu	RNA-binding protei	glycine-rich prote	fus-like protein -	eggshell protein p	glycine-rich RNA-b	glycine-rich prote	glycine-rich prote	prote	glycine-rich prote
SUMMARIES	ΩI	T04592	KNRZG1	S54729	T03583	T29282	T49109	T07381	S71795	T31503	B84777	S12312	S31415	T20410	S12311	T24045	F84797	S71779	A26099	T10479	833798	833799	S01821	G02127	A44805	S41772	S20846	KNNT2S	849193	S14857
	DB	2	Н	~	~	7	7	~	~	7	7	7	-	7	~	~	~	0	-	~	4	-	Н	7	7	~	7	٦	7	Н
	Query Match Length	221	165	404	165	136	396	207	440	285	255	168	291	385	142	1226	106	167	384	162	462	526	252	528	220	148	155	_	m	157
a	Query Match	74.2	68.8	9.89	68.3	68.1	67.8	66.4	66.1	62.9	65.8	65.3	65.3	64.9	64.8	64.4	64.3	64.1	63.9	63.6	63.6	63.6	63.4	63.4	63.1	62.8	62.8		62.8	62.6
	Score	221	205	204.5	203.5	203	202	198	197	196.5	196	194.5	194.5	193.5	193	192	191.5	191	190.5	189.5	189.5	189.5	189	189	188	187	187	187	187	186.5
	Result No.	٦	7	٣	4	Ŋ	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

acp-22 protein - y	acp-22 protein - y	glycine-rich prote	embryonic abundant	hypothetical prote	glycine-rich RNA-b	glycine-rich prote	calpain (EC 3.4.22	hypothetical prote	hypothetical prote	glycine-rich RNA-b	RNA binding protei	glycine-rich prote	glycin-rich protei	hypothetical prote	glycine-rich RNA-b
063	224	999	536	1268	8331	110465	HOL	4470	0799	1771	3050	9774	7483	155	1453
816	832	834	S04	120	83	Ħ	IJ	ဗ	ဦ	S4	35	S	85	AB	S7.
2 816	2 8323	2 \$34(	2 S04	2 T2(	1 53	2 T1	1 CI	2 C8	2 T0	2 S4	2 85	2 81	2 85	2 AB2	2 87
~	199 2 832	7	03	2	٦,	2	-	~	2	2	7	7	7	7	7
~	199 2 8	271 2 8	157 2 8	393 2 7	169 1 8	169 2 7	268 1 (	302 2 (	201 2 1	156 2 8	173 2 8	82 2 8	7	681 2 7	161 2 8
62.6 199 2 8	199 2 8	62.6 271 2 8	62.2 157 2 8	62.2 393 2 7	61.9 169 1 8	61.4 169 2 7	61.4 268 1 (	61.2 302 2 (	61.1 201 2 1	60.7 156 2 8	60.7 173 2 8	60.6 82 2 8	408 2 8	60.6 681 2 #	60.4 161 2 8

## ALIGNMENTS

RESULT 1

. H

	1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
	T04592
	glycine-rich cell wall structural protein homolog F23E13.120 - Arabidopsis thaliana
	C;Species: Arabidopsis thaliana (mouse-ear cress)
	C;Date: 23-Apr-1999 #sequence revision 23-Apr-1999 #text change 09-Jul-2004
	C;Accession: T04592
	R; Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Jesse, 7
	submitted to the Protein Sequence Database, March 1998
	A; Reference number: Z15378
	A; Accession: T04592
	A; Molecule type: DNA
	A;Residues: 1-221 <bev></bev>
	A; Cross-references: UNIPROT: 065514; EMBL: AL022141
	A; Experimental source: cultivar Columbia; BAC clone F23E13
	C, Genetics:
	A;Map position: 4
•	A,Note: F23E13.120
	Similarity 55.8%;
	Matches 43; Conservative 0; Mismatches 8; Indels 26; Gaps 1;
	Qy 1 GGGGGGGGGGGGGGGGGGGGGGGGGGGGG
	Db 98 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
	Qy 35 GGGGGGGGGGG 51
	Db 158 GGGGGGGGGGGGG 174

Richi, M.; Wu, R.
Plant Mol. Biol. 16, 187-198, 1991
Aritle: A novel glycine-rich cell wall protein gene in rice.
A;Reference number: \$13385; MUD:91370862; PMID:1716496
A;Accession: \$13385
A;Accession: \$13385
A;Molecule type: DNA
A;Residues: 1-165 <LEI>
A;Cross-references: UNIPROT:P25074; EMBL:X53596; NID:g20246; PIDN:CAA37665.1; PID:g20247
C;Genetics: glycine-rich cell wall structural protein 1 precursor (clone lambda-313) - rice C;Species: Oryza sativa (rice) C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004 C;Accession: S13385

A,Gene: grp-1 C;Superfamily: glycine-rich cell wall structural protein 1 C;Keywords: cell wall; duplication; structural protein F;1-23/Domain: signal sequence #status predicted <SIG> F;24-165/Product: glycine-rich cell wall structural protein 1 #status predicted <MAT> F;30-55/Region: repeat R1

'n

```
A;Cross-references: UNIPROT:024184; EMBL:AF009411; NID:g2267592; PIDN:AAB63589.1; PID:g22
A;Experimental source: cv. Milyang 23
C;Superfamily: glycine-rich RNA-binding protein; ribonucleoprotein repeat homology
F;9-76/Domain: ribonucleoprotein repeat homology <RRM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q18444; EMBL:US8755; PIDN:AAB00696.1; GSPDB:GN00022; CESP:C3*
A;Experimental source: strain Bristol N2; clone C34D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-396 <BEV>
A;Cross-references: UNIPROT:065450; EMBL.AL022140; GSPDB:GN00062; ATSP:AT4g22020
A;Experimental source: cultivar Columbia; BAC clone F1N20
                                                                                                                                                                                                                                                                                                                                                                                      CiSpecies: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Âlternate nâmes: protein AT4G22020
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                        Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 202; DB 2; Length 396;
Pred. No. 1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: Phaseolus glycine-rich cell wall protein 1.8
                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Du, Z.; Le, T.T.
submitted to the EMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid C34D4
A;Reference number: Z20600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein C34D4.11 - Caenorhabditis elegans
                                                                                                                                                                                             DB 2;
                                                                                                                                                                                   Score 203.5; DB 2.
Pred. No. 4.2e-10;
0; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 74.5%; Pred. No. 4.1e-10;
Matches 38; Conservative 0; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-136 <DUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 4
A;Introns: 20/1; 66/1; 98/1; 116/1
C;Superfamily: Arabidopsis glycine-rich protein 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycine-rich protein - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.8%;
                                                                                                                                                                                         Query Match
Best Local Similarity 68.9%;
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
   A;Residues: 1-165 <LEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: ATSP:AT4g22020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Gene: CESP:C34D4.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: T29282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 G 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: T49109
                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 G S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                   유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                              ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycine-rich RNA-binding protein - rice (5) Species: Oryza sativa (rice) (5) Species: Oryza sativa (rice) (5) Species: Oryza sativa (rice) (5) Species: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004 (5) Accession: T03893 (6) Accession: T03893 (7) B.Y.; Lee, J.S.; Eun, M.Y. Rylee, M.C.; Kim, C.S.; Yi, B.Y.; Lee, J.S.; Eun, M.Y. A; Description: Isolation and characterization of RNA-binding glycine rich protein of rich A; Reference number: 214958 (7) A; Rocession: T03893 (7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-404 <STO>
A; Residues: 1-404 <STO>
A; Residues: 1-404 <STO>
A; Residues: 1-404 <STO>
A; Cross-references: UNTRROT: 027294; EMBL: L37083; NID: 9567105; PIDN: AAC41563.1; PID: 95671
B; Stolow, D.T.; Haynes, S.R.
Nucleic Acids Res. 23, 835-843, 1995
A; Title: Cabeza, a Drosophila gene encoding a novel RNA binding protein, shares homology A; Reference number: $54728; MUID: 95223793; PMID: 7708500
                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 GGGGGGGRGGFGGRRGGGGGGGGGGGRFD----RGGGGGGNGGGGGRYDRGGGG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---GGGG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 404;
                                                                                                                                                                                                                       Score 205; DB 1; Length 165; Pred. No. 3.2e-10;
                                                                                                                                                                                                                                                                                          13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Cross-references: FlyBase: FBgn0011571
(S. Superfemily: ribonucleoprotein repeat homology
C; Keywords: RNA binding
F;120-195/Domain: ribonucleoprotein repeat homology <RRM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 68.6%; Score 204.5; DB 2. Local Similarity 66.7%; Pred. No. 6.6e-10; Nee 42; Conservative 0; Mismatches 4.
                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                          68.8%; Score 205; 72.5%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 118-203;273-310 <STW>
A;Cross-references: EMBL:L37083
                                                                                                                                                                                                                                                        Best Local Similarity 72.5
Matches 37; Conservative
                                                                                      F)100-131/Region: repeat R1
F)132-138/Region: repeat R2
F)139-160/Region: repeat R1
F;56-62/Region: repeat R2
F;62-92/Region: repeat R1
F;93-99/Region: repeat R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269
                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T03583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                 요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                         ઠ
```

ô

m

ä

```
Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; i M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-168 < CRE>
A; Cross-references: University of the matter of two additional Gly are shown after 110-Gly
C; Superfamily: glycine-rich RNA-binding protein; ribonucleoprotein repeat homology
C; Keywords: GTP binding
F; 9-76/Domain: ribonucleoprotein repeat homology < RRMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q9SIH2; GB:AE002093; NID:g4678224; PIDN:AAD26969.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homology
                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Roseidues: 1-288 - 4WIL>
A;Cross-references: UNIPROT: 09UZU0; EMBL;AL117204; PIDN: CAB55137.1; CESP: Y116A8C.35
A;Experimental source: clone Y116A8C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A,Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein At2g36120 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Sorghum bicolor (sorghum)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGGGGGGGGGGGGGG--GGGYGRKKRRQRRRGGGGG----GGGGGGGGGGGGGG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGGGGGGGGGGGGGGGGY-GRKKRRQRRRGGGGGGGGGGGGGGGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.3%; Score 194.5; DB 1; Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cydcossion: S1232
Cydcossion: S1232
RyCretin, C.; Puigdomenech, P.
Plant Mol. Biol. 15, 783-785, 1990
A;Title: Glycine-rich RNA-binding proteins from Sorghum vulgare.
A;Reference number: S12311; MUID:91346715; PMID:1715211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 196.5; DB 2;
Pred. No. 2.2e-09;
1; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycine-rich RNA-binding protein (clone S2) - sorghum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 196; DB 2;
Pred. No. 2.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
   R.WcMurray, A.
submitted to the EMBL Data Library, October 1999
A.Reference number: 221041
                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.9%;
ilarity 73.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 68.4%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                      A; Gene: CESP: Y116A8C.35
A; Introns: 31/3; 143/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-255 <STO>
                                                                                                          A, Accession: T31503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: B84777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: S12312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: At2g36120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                             C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                     Glycine-rich protein Tfm5 - tomato
Glycine-lyopersaicon esculentum (tomato)
Glycine: Lycopersaicon esculentum (tomato)
Glycine: Lycopersaicon esculentum (tomato)
Glycine: Lycopersaicon (Glycine)
Glycine: T07381
Alitle: Developmental and transgenic analysis of two tomato fruit enhanced genes.
Alitle: Developmental and transgenic analysis of two tomato fruit enhanced genes.
Alitle: Developmental and transgenic analysis of two tomato fruit enhanced genes.
Alitle: Developmental and transgenic analysis of two tomato fruit enhanced genes.
Alitle: Developmental and transgenic analysis of two tomato fruit enhanced genes.
Alitle: Developmental and transgenic analysis of two tomato fruit enhanced genes.
Alitle: Developmental and transgenic analysis of two tomato fruit enhanced genes.
Alitle: Developmental and transgenic analysis of two tomato fruit enhanced genes.
Alitle: Developmental and transgenic analysis of two tomato fruit enhanced genes.
Alitle: Developmental and transgenic analysis of two tomato fruit enhanced genes.
Alitle: Developmental and transgenic analysis of two tomato fruit enhanced genes.
Alitle: Developmental and transgenic analysis of two tomato fruit enhanced genes.
Alitle: Developmental and transgenic analysis of two tomato fruit enhanced genes.
Alitle: Developmental and transgenic analysis of two tomato fruit enhanced genes.
Alitle: Developmental and transgenic analysis of two tomato fruit enhanced genes.
Alitle: Developmental and transgenic analysis of two tomato fruit enhanced genes.
Alitle: Developmental and transgenic analysis of two tomato fruit enhanced genes.
Alitle: Developmental and transgenic analysis of two tomato fruit enhanced genes.
Alitle: Developmental and transgenic analysis of two tomato fruit enhanced genes.
Alitle: Developmental analysis of two tomato fruit enhanced genes.
Alitle: Developmental enhanced genes.
Alitle: Developmental enhanced g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcription factor CBF-2 - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 16-Aug-2004
C;Accession: S71795
R;Yuasa, J.; Hirano, S.; Yamagata, M.; Noda, M.
Nature 382, 632-635, 1996
A;Tile: Visual projection map specified by topographic expression of transcription fact A;Reference number: S71794; MUID:96338226; PMID:8757134
A;Accession: S71795
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-440 <VUA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q98937; EMBL:U47276; NID:g1546783; PIDN:AAB08467.1; PID:g154
C;Superfamily: fork head DNA-binding domain homology
F;143-234/Domain: fork head DNA-binding domain homology <FHD>
       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Y116A8C.35 - Caenorhabditis elegans
C;Species: Cenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Indels 10; Gaps
                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Indels
   15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.4%; Score 198; DB 2;
ilarity 70.6%; Pred. No. 1.4e-09;
Conservative 0; Mismatches 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 66.1%; Score 197; DB 2; Best Local Similarity 63.9%; Pred. No. 2.8e-09; Matches 39; Conservative 1; Mismatches 11.
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: cultivar UC82b; fruit C, Genetics: A; Gene: Tfms C, Superfamily: hydroxyproline-rich glycoprotein
   ö
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 G 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 G 51
36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
```

ä

us-09-910-432-20.rpr

```
completed: September 7, 2005, 13:00:51
he : 24 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search cor
Job time
                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                      RESULT 12
$31415
glycine-rich protein GRP22 - rape
glycine-rich protein GRP22 - rape
Glybcine-rich protein GRP22 - rape
Glybcines: Brassica napus (rape)
Clybcies: Brassica napus (rape)
Clybcies: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
Clybcieslon: 31415
Ribergeron, D.; Bolvin, R.; Baszczynski, C.L.; Bellemare, G.
submitted to the EMBL Data Library, August 1992
Albescription: Characterization and expression of a gene family encoding glycine-rich pr
                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Accession: S31415
A,Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-291 <BRA
A,Residues: 1-291 <BRA
A,Cross-references: UNIPROT:Q39337; EMBL:Z15045; NID:g17820; PIDN:CAA78762.1; PID:g17821
C,Superfamily: Phaseolus glycine-rich cell wall protein 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q93424; EMBL:Z81053; PIDN:CAB02877.1; GSPDB:GN00023; CESP:Ed
A;Experimental source: clone E02A10
                         <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
T20410
T20410
T20410
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T20410
S;Accession: T20410
R;Thomas, K.
submitted to the EMBL Data Library, October 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGGGGGGGGG-----GGGGGGYGRKKRRQRRRGGGGGGGGGGGGGGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGGGGGGGGGGGGG----GGGYGRKKRRQRRRGGGGG----GGGGGGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                         19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 54.9%; Score 193.5; DB 2; Length 385; Similarity 72.5%; Pred. No. 4.8e-09; Conservative 0; Mismatches 5; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 291;
  Pred. No. 2.2e-09;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 194.5; DB 1; Length
Pred. No. 3.3e-09;
0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: 219271
A;Accession: T20410
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C,Genetics:
A,Gene: CESP:E02Al0.2
A,Map position: 5
A,Introns: 32/1; 72/1; 85/1; 122/1; 133/1; 220/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 65.3%;
Local Similarity 65.0%;
hes 39; Conservative
    63.1%;
Best Local Similarity 63.1
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S31415
                                                                                                                                                                                  EGGGG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-385 <WIL>
                                                                                                                                            -6666 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ma.
Local Sim.
37;
                                                                                                                                            48
                                                                                                                                                                                    144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
                                                                                              셤
                                                                                                                                          ò
                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
```

```
A/Accession: S12311
A/Molecule type: mRNA
A/Residues: 1-142 CCRE
A/Residues: 1-142 CCRE
A/Note: the authors translated the codon ACG for residue 37 as Ser and CGC for residue 54
A/Note: the authors did not translate the codons for residues 92 and 93
C/Superfamily: glycine-rich RNA-binding protein; ribonucleoprotein repeat homology
C/Reywords: RNA binding
F;1-55/Domain: ribonucleoprotein repeat homology (fragment) <RRMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residuss: 1-1226 <WLL>
A,Residuss: 1-1226 <WLL>
A,Cross-references: UNIPROT:Q21835; EMBL:Z68008; PIDN:CAA92000.1; GSPDB:GN00028; CESP:R08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: X
A;Introns: 53/2; 113/1; 152/3; 204/3; 272/1; 354/1; 389/3; 714/3; 839/3; 877/1; 960/3; 1(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein R08B4.1 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C.Accession: T24045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1226;
                                                                                                                                                                                                                                                                                                                                                                                                    ch 64.8%; Score 193; DB 2; Length 142;
1. Similarity 70.9%; Pred. No. 2.6e-09;
39; Conservative 0; Mismatches 6; Indels
Plant Mol. Biol. 15, 783-785, 1990
A;Title: Glycine-rich RNA-binding proteins from Sorghum vulgare.
A;Reference number: S12311; MUID:91346715; PMID:1715211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 64.4%; Score 192; DB 2; Local Similarity 66.7%; Pred. No. 1.4e-08; les 34; Conservative 0; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Experimental source: clone R08B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: Z19834
A;Accession: T24045
                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: CESP:R08B4.1
```

```
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

OM protein - protein search, using sw model

September Run on:

7, 2005, 12:47:19; Search time 112.5 Seconds (without alignments) 232.143 Million cell updates/sec

Title: Perfect score:

Sequence:

51

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

Total number of hits satisfying chosen parameters:

1612378

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	ption	oryza sativ	arabidopsis	burkholderi	oryza sativ	oryza sativ	arabidopsis	oryza sativ	oryza sativ	caenorhabdi	arabidopsis	oryza sativ	ectocarpus	drosophila	drosophila	drosophila	drosophila	lycopersico	picea glauc	oryza sativ	gallus gall	oncorhynchu	oryza sativ	caenorhabdi	oryza sativ	drosophila	arabidopsis	plasmodium	rhizobium m	gallus gall	drosophila	drosophila
	Description	Q69xv3	065514	Q62fe6	Q852i5	P25074	Q918n6	024184	Q75hg8	018444	065450	0942q2	08qkx8	Q95ux2	Q9w1v3	Q8i1f4	027294	043522	Q9xe14	Q69t79	098937	Q90w75	022385	09n2n0	Q6z142	095uw6	Q9sih2	015647	Q92p87	042403	Q95ux4	Ogsnrk
ğ		, , , , ,																														
SUMMAKIES	ai	069XV3	065514	Q62FE6	085215	GRP1 ORYSA	9NS160	024184	Q75HG8	Q18444	065450	094202	Q8QKX8	Q95UX2	FBRL DROME	FBRL_DROER	CAZ DROME	043522	Q9XEL4	Q69T79	FXGA_CHICK	Q90W75	022385	Q9U2U0	062142	Q95UW6	Q9SIH2	015647	Q92P87	042403	Q95UX4	AGNER
	DB	10	~	~	~	-	~	~	~	~	~	~	N	0	-4	-	-	7	~	7	н	7	7	~	7	7	~	7	~	~	7	c
	Query Match Length	321	221	199	329	165	175	165	551	136	396	535	698	165	344	345	399	207	155	239	440	592	161	285	422	161	255	301	192	344	163	165
a	Query Match	78.5	74.2	72.0	70.3	68.8	9.89	68.3	68.3	68.1	67.8	67.3	67.3	66.8	8.99	8.99	9.99	66.4	66.1	66.1	66.1	66.1	62.9	62.9	65.9	65.8	65.8	65.8	9.59	65.4	65.3	5,5
	Score	234	221	214.5	209.5	205	204.5	203.5	203.5	203	202	200.5	200.5	199	199	199	198.5	198	197	197	197	197	196.5	196.5	196.5	196	196	196	195.5	195	194.5	194.5
	Result No.	1	7	٣	4	ß	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25		2 <b>M</b>	G CV	6	e F	-

[1] — SEQUENCE FROM N.A. Braun M., Holzer E., Brandt A., Duesterhoeft A., Bevan M., Hilbert H., Braun M., Holzer E., Mewes H.W., Mayer K., Hoheisel J., Jesse T., Heijnen L., Vos P., Mewes H.W., Mayer K., Schueller C.; Schueller C.; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

[2] SEQUENCE FROM N.A.

01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative glycine-rich cell wall protein.
Name=F23R13.120, Synonyma=AT4936230;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

221 AA.

PRT;

PRELIMINARY;

065514 065514;

RESULT 2

065514

Q99p44 drosophila Q99070 sorghum bic Q81pa7 triticum ae Q75qn8 triticum ae Q39337 brassica na Q9grw7 drosophila Q23934 oryza sativ Q6asx7 oryza sativ Q6asx7 oryza sativ Q9fud5 sorghum bic Q7v9d6 prochloroco Q97nu7 rhizobium m Q93424 caenorhabdi Q81519 plasmodium Q99069 sorghum bic		PRELIMINARY; PRT; 321 AA.  269XV3; 269XV3; 26-CCT-2004 (TrEMBLrel. 28, Created) 25-CCT-2004 (TrEMBLrel. 28, Last sequence update) 25-CCT-2004 (TrEMBLrel. 28, Last annotation update) 25-CCT-2004 (TrEMBLrel. 28, Last annotation) 26-CT-2004 (TrEMBLrel. 28, Last annotation) 26-CT-2004 (TrEMBLrel. 28, Last annotation) 27-CT-2004 (TrEMBLrel. 20, Last annotation) 25-CT-2004 (TREMBLR	8 2; 8-12; 3GGGGG        3GGGGG
Q9GP44 GRP2_SORBI Q8LPA7 Q8LPA7 Q939337 Q9GRW7 Q2384 Q6ASX7 Q9FUD5 Q9YUD5 Q92NU7 Q93424 Q81519 GRP1_SORBI	ALIGNMENTS	ELIMINARY; FRT; 321 AA.  TEMBLE-1. 28, Created) TEMBLE-1. 29, Last sequence update) TEMBLE-1. 28, Last annotation updat Toe-rich cell wall structural protei Japonica cultivar-group)  Idiplantae; Streptophyta; Embryophy Magnoliophyta; Liliopsida; Poales; Oryzeae; Oryza.  N.A.  N.A.  N.A.  N.A.  NIPA TY	isma isma KRRQ
65.3 165 2 65.3 168 1 65.3 229 2 65.3 231 2 65.3 291 2 65.1 162 2 65.1 162 2 64.9 170 2 64.9 233 2 64.9 2359 2 64.9 2359 2		93 PRELIMINARY; PRT; 321 AA. 2695V3; 26-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) 26-OCT-2004 (TREMBLRel. 28, Last annotation update) 26-OCT-2004 (TREMBLRel. 28, Last annotation update) 26-OCT-2004 (TREMBLRel. 28, Last annotation update) 27-OCT-2004 (TREMBLRel. 28, Last annotation update) 27-OCT-2004 (TREMBLRel. 28, Last annotation update) 28-OCT-2004 (TREMBLRel. 28, Last anno	Similarity 82.4%; Pred 2; Conservative 0; M GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
32 194.5 34 194.5 35 194.5 36 194.5 37 194.5 38 194.5 40 193.5 42 193.5 42 193.5 44 193.5	RESULT 1 O69XV3	Q69XV3 AC 069XV3; DT 25-0CT-2004 (TERMB NAME-ED040H10.37) OS GLARATCOIGNE, VITIGIA, OS GLARATCOIGNE, OS GLARATCOIGNE, OS GLARATCOIGNE, OX MOBIL TAXID=39947; RN 5RQUENCE FROM N.A. RA SASAKI T., MATSUMON RT "ONYZA SATIVA NIBUMATCOIGNE, ON THE SAGUENCE FROM N.A. RA SASAKI T., MATSUMON RT "ONYZA SATIVA NIBUMATCOIGNE, ON THE SAGUENCE TO THE SA	Query March Best Local Sim Marches 42; Qy 1 GG Db 99 GG

```
NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4530;
                                                                               01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=GRP-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buell R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
GRP1_ORYSA
     085215
                                    요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGGGGGGGGGGG-----GGGGGGGYGRKKRRQRRRGGG----GGGG-----GGGGGGGGG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nierman W.C., Deshazer D., Kim H.S., Tettelin H., Nelson K.E., Feldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C., Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M., Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N., Structural flexibility in the Burkholderia mallei genome."; "Structural flexibility in the Burkholderia mallei genome."; EMEL, CP000010; Aaul6078.1; 101:14247-14251(2004).

SEQUENCE 199 AA; 19605 MW; 39022C03692C8DB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------GGGGGGGGGGGGYGRKKRRQRRRGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burkholderia mallei ATCC 23344.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 214.5; DB 2; Length 199;
Pred. No. 1.5e-10;
                                                                       SEQUENCE FROM N.A.
Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.2%; Score 221; DB 2; Length 221; 55.8%; Pred. No. 4.8e-11; ive 0; Mismatches 8; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Indels
EU Arabidopsis sequencing project;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                             EU Arabidopsis sequencing project;
Submitred (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO22141; CAA18129.1; --.
EMBL; AL051589; CAB802294.1; --.
                                                                                                                                                                                                                                                                                                                                                                                           SSHELL.
20344 MW; DEBDAE2E2C57A9F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                              PIR; T04592; T04592.
INTerPro; IPR002952; Eggehell.
PRINTS; PR01228; EGGSHELL.
SEQUENCE 221 AA; 20344 NW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single-strand binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 GGGGGGGGGGGGG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 GGGGGGGGGGGGG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=ssb; ORFNames=BMA3093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 55.8
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                   FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=243160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ATCC 23344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 GGGG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 GGGG 51
                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q62FE6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
062FE6
1062FE6
1062FE7
AC 062FE7
DT 25-C
DT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              유
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bitchiformatics and the EMBL outstation - the Buropan Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lei M., Wu R.;
"A novel glycine-rich cell wall protein gene in rice.";
Plant Mol. Biol. 16:187-198(1991).
--- FUNCTION: Responsible for plasticity of the cell wall (Potential).
--- SUBCELLULAR LOCATION: Cell wall (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Buell C.R., Yuan O., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.

Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Wang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
White O., Salzberg S.L., Fraser C.M.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                      Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Enthartoldeae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ب
•
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gramens, 085215; -.
Hypothetical protein.
SEOURNCE 329 AA; 33756 MW; 0530227C1F442C71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
Glycine-rich cell wall structural protein 1 precursor.
                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.3%; Score 209.5; DB 2
75.5%; Pred. No. 5.8e-10;
329 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                01-JUN-2003 (TrEMBLrel. 24, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
Hypothetical protein OSJNBa0078A17.2
Hame-OSJNBa0078A17.2;
                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-cv. Indica / IR36;
MEDLINE-91370862; PubMed=1716496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X53596; CAA37665.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AC091532; AA038820.1;
                                           (TrEMBLrel, 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
```

ω ..

us-09-910-432-20.rup

```
Q18444
Q18444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q75HG8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
Q75HG8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q18444
   SURBERRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOOR READ THE READ TO THE READ THE READ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Potential.
Glycine-rich cell wall structural protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:K14Al7.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGGGGGGGGGGGGGG-----GYGRKKRRQRRRGGGGGGGGGGGGGGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glycine-rich RNA-binding protein.
Oryza sativa (Rice).
Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales; Poaceae; Ehrhartoideee, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 dsadadadadadadadagasdsayayayayakadadadadadadadadadada 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata
Submitted (Apr.1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AB026636; BAA94989.1; -
SEQUENCE 175 AA; 14340 MW; CC7CD9918498707C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.8%; Score 205; DB 1; Length 165; llarity 72.5%; Pred. No. 7.5e-10; Conservative 1; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 204.5; DB 2; Length
Pred. No. 8.6e-10;
0; Mismatches 12; Indels
                                                                                                                                                                               Gly-rich.
R2 (Tyr-rich).
R2 (Tyr-rich).
R2 (Tyr-rich).
W, E36CE31C3650AC9A.CRC64,
         Gramene; P25074; -.
Cell wall; Repeat; Signal; Structural protein.
SIGNAL 1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=20277480; PubMed=10819329;
                                                                                                                                                                               159 GI
62 R2
99 R2
138 R2
13536 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.6%;
67.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Res. 7:131-135(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
PIR; S13385; KNRZG1.
                                                                                                                                                                               31 1
56
93
132 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
ses 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakamura Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clones.";
                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             024184
024184;
                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                   REPEAT
                                                                                                                    CHAIN
                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
0915/8/6
0915/8/6
DD 01-0
DD 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RANTITITIES
STITITIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
90 dedededesegredesegredesegredededesegre----prrederedededededeseg 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Putative prohibitin.
Name-OSJNBa0024F18.27;
Norza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                      Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
STRAIN=Milyang 23;
Liee M.C., Kim C.S., Yi B.Y., Lee J.S., Eun M.Y.;
Submitted (UVI.1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF009411, AAB63589.1; -.
PIR, T03583, T03583.
HSSP, Q61474, 1UAW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buell R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                  Diametro; Carray, RNA_rec_mot.
Pfam; PF00076; RRM 1; 1.
SMART; SM00360; RRM; 1.
PROSTIE; PS50102; RRM; 1.
PROSTIE; PS501030; RRM; 1.
PROSTIE; PS501030; RRM RNP 1; UNKNOWN 1.
SRQUENCE 165 AA; 16334 MW; 8ABDADBCIC81EC21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59192 MW; 34C1EC87BB3CA297 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 68.3%; Score 203.5; DB 2; Best Local Similarity 72.5%; Pred. No. 2.7e-09; Matches 37; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                    68.3%; Score 203.5; DB 2, 68.9%; Pred. No. 9.9e-10; iive 0; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       551 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AC135594; AAR89849.1;
InterPro; IPR001107; Band_7.
Pfam; PF01145; Band_7; 1.
SEQUENCE 551 AA; 59192 MW
                                                                                                                                                                                                                                                                                                                                                      Query Match 68.3
Best Local Similarity 68.9
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 G 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 G 51
```

ï

ö

Gaps

51 ö

SO WE RECOVER THE REPORT OF THE REAL PROPERTY OF THE PROPERTY

```
PEDURNCE FROM N.A.

SEGURNCE FROM N.A.

SERAÍT., MATSUMOLO T., Yanamoto K., Sakata K., Baba T., Katayose Y., Rasaki T., Matsumoto T., Yanamoto K., Sakata K., Baba T., Katayose Y., Anu J., Nimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H., Anu J., Nimura Y., Chiden Y., Hayashi M., Okamoto M., Ando T., Acki H., Arita K., Hamada M., Harada C., Anijima M., Itoha M., Itoha Y., Idonuma A., Iijima M., Ikeda M., Anishana M., Itoh Y., Itoha Y., Itoha Y., Kamiya K., Anasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I., Marai Y., Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Mukai Y., Nakamichi Y., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M., Animokawa T., Shomura A., Song J., Takazaki Y., Tarasawa K., Tsuji K., Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Yano M., Jiang J., Golobori T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
P0701D05.1 protein (B1189A09.32 protein).
Name=P0701D05.1; Synonyms=B1189A09.32;
Oryza sativa (Japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.

Wedler H., Wambutt R., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AL022140; CAA18105.1; -.

EMBL: AL161556; CAB79157.1; -.
                                                                                                                                                                                                                                                                                                                  67.8%; Score 202; DB 2; Length 396; 70.6%; Pred. No. 2.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The genome sequence and structure of rice chromosome 1."; Nature 420:312-316(2002).
                                                                                                                                                                                                                                                                                                                                        Pred. No. 2.7e-09;
0; Mismatches 15; Indels
                                           EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMAKY; PSC0102; REM; 1.
PROSITE; PSC0102; REM; 1.
PROSITE; PSC01358; ZF RANBP2_1; 1.
PROSITE; PSC0199; ZF RANBP2_2; 1.
REOUENCE 535 AA; 50911 MW; 72B93AE30AD8E041 CRC64;
                                                                                                                                                                                                                               InterPro; IPR002173; PEKB.
PROSITE; PS00583; PPKB KINASES 1; UNKNOWN 1.
SEQUENCE 396 AA; 31470 MW; TCDCD0FFBE337CAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002952; Eggshell.
InterPro; IPR000504; RNA_rec_mot.
InterPro; IPR001876; Znf_RanGDP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP003301; BAB64787.1; -. EMBL; AP003209; BAC00578.1; -. HSSP; O95218; INOZ.
                                                                                                                                                                                                                                                                                                                                        70.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00076; RRM 1; 1.
Pfam; PF00641; zf-RanBP; 1.
PRINTS; PR01228; EGGSHELL.
SMART; SM0350; RRM; 1.
                                                                                                                                                                                                                                                                                                                                      Local Similarity 70.6 tes 36, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gramene; 094202;
                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  094202
                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
Q942Q2
    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Mame-AT4922020;
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TAXID=3702;
                                                                                                                 Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Bevan M., Wedler H., Wambutt R., Bancroft I., Mewes H.W., Lemcke K.,
Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 Gánddedandedekededededekedededekedededekededekedekedede 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 203; DB 2; Length 136;
Pred. No. 9.3e-10;
0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Du Z., Le T.T.;
"The sequence of C. elegans cosmid C34D4.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WormDep; C34D4.11.
WormDep; C34D4.11.
WormDep; C34D4.11; CE17505.
Hypothetical protein.
SEQUENCE 136 AA; 12294 MW; F72778C4EA5648B5 CRC64;
               01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Hypothetial protein C34D4.11.
Name=C34D4.11; ORFNames=C34D4.11;
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396 AA
(TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                             STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
WormBase Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 68.1%;
1 Similarity 74.5%;
38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston R.;
Submitted (NOV-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Bristol N2; Wilson R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Bristol N2;
                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       065450
```

RESULT 10 O65450

ઠે 유 

```
셤
                                                                                                                                                                8
                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=E8V-1;
Delaroque N., Bothe G., Pohl T., Knippers R., Mueller D.G., Boland W.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF204951; AAF28325.1;
SEQUENCE 698 AA; 74035 MW; C7638DDB922E0D50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Delaroque N., Wolf S., Muller D.G., Knippers R.; "Characterization and immunolocalization of major structural proteins
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                           Ectocarpus siliculosus virus.
Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phaeovirus.
                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20192171; PubMed=10725207; DOI=10.1006/viro.2000.0225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila virilis (Fruit fly).
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta, Pterygota,
Neoptera, Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea, Drosophilidae, Drosophila.
     DB 2; Length 535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Huttunen S., Vieira J., Hoikkala A., Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AY012591; AAG48861.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -.
I; C7638DDB922E0D50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15822 MW; F0D87E1E78DCC01F CRC64;
                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -DEC-2001 (TrEMBLrel. 19, Last sequence update)
-OCT-2002 (TrEMBLrel. 22, Last annotation update)
on or off transient A (Fragment).
Score 200.5; DB 2.
Pred. No. 4.6e-09;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.3%; Score 200.5; DB 2
68.4%; Pred. No. 5.8e-09;
ive 0; Mismatches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 AA.
                                                                                                                                                                                                                                                                                                  698 AA
                                                                                                                                                             72 GGGGGGYGGGGGGGGGGGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q95UX2;
01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in the brown algal virus E8V-1.";
Virology 269:148-155(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase; FBgn0042729; Dvir\nonA
     67.3%;
                              68.48;
                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 68.4
les 39; Conservative
                                                       39; Conservative
                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=37665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=ORF 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001
01-OCT-2002
No on or off
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=SBB;
                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002
     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                             080KX8
                                                                                                                                                                                                                                                                                               080KX8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 095UX2
                                                                                                                                                                                                                                           RESULT 12
Q8QKX8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
095UX2
AC 095UX2
AC 095UX
DT 01-DE
DT 
                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                          요
                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                              ઠે
```

```
RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Worteran J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Henderson S.N.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Beson K.Y., Beans D.W., Berman B.P., Bhandari D., Bolshakov S.,
Burtis C., Busam D.A., Burtler H., Cadieu E., Center A., Chandra I.,
RA Burtis J.M., Canley S., Dahlke C., Davenport L.B., Davies P.,
RA Burtis S., Delcher A., Deng Z., Mays A.D., Davies P.,
RA Burtis S., Delcher A., Deng Z., Mays A.D., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Netchun K.J.,
RA Glodek A., Gong F. Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Liasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
Raluml B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
Raluml B.E., Molfras C.D., Kraft C., Morris J., Moshrefi A.,
Raluml B.E., Wolfen W., Murphy B., Murphy L., Murzny D.M., Nelson D.L.,
Raleson R., Wolson K.A., Nixon K., Nusskern D.R., Parish T.,
Shue B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Snith T.,
Shue B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Snith T.,
Rang Z.-Y., Wassarman D.A., Wallscock G. W., Waissenband J.,
Rang Z.-Y., Wassarman D.A., Wallscock G. W., Waissenband J.,
Rang Z.-Y., Wassarman D.A., Wallscock G. W., Waissenband J.,
Rang X.-Y., Wassarman D.A., Wallscock G. W., Waissenband J.,
Rang X.-Y., Wassarman D.A., Wallscock G. W., Wallscock G. Zhon R.,
Rang X.-Y., Wassarman D.A., Wallscock G. W., Wallscock G. Wallshill M., Scheeler F., Short H.,
Rang X.-Y., Wassarman D.A., Wallscock G. W., Wallscock G. Wallscock G. Wallscock G. Wallscock G. Wallscock G. Wallsco
                                                                         <u>ښ</u>
                                                                                                                                                                                                                    ---- edgegegegegerdring 115
                                                                                                                                           MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
                                                                         22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
64.5%; Pred. No. 2.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9W173; Q24348; QBIGKS;
25-JAN-2005 (Rel. 46, Created)
25-JAN-2005 (Rel. 46, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                        67 GGGGGGGGGGGGGGGGGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 287:2185-2195(2000)
                                                                         40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENOME REANNOTATION.
                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               116 dd 117
                                                                                                                                                                                                                                                                                             50 GG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fibrillarin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
FBRL_DROME
                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HID DIT TO THE SECOND OF THE S
```

φ

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lbb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Berkeley; TISSUE=Embryo;
MEDLINE=22426066; PubMed=12537569;
Stapleton M., Carlson J.W., Broketein P., Yu C., Champe M.,
George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
Rubin G.M., Celniker S.E.;
"A Drosophila full-length cDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8
                                                                                                                                                                                                                                                                                                                                         Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stableton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: By homology to other fibrillarins, some or all of the N-terminal domain arginines are modified to asymmetric dimethylarginine (DMA) [8y similarity).

SIMILARITY: Belongs to the fibrillarin family.

CAUTION: Ref.4 sequence differs from that shown due to erroneous gene model prediction and to a frameshift in position 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Asymmetric dimethylarginine (By similarity).
Asymmetric dimethylarginine (Probable).
Asymmetric dimethylarginine (Probable).
                                                                        Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asymmetric dimethylarginine (By similarity)
Asymmetric dimethylarginine (By similarity)
Asymmetric dimethylarginine (By similarity)
Asymmetric dimethylarginine (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRODO52; FIBRILLARIN.
PRODOM; PD004637; FIBRILLARIN; 1.
PROSITE; PS00566; FIBRILLARIN; 1.
Methylation; Nuclear protein; Ribonucleoprotein; RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (By
                                                                                                                                                                                                                                                                 SEQUENCE OF 5-140 FROM N.A.
MEDLINE=87230988; PubMed=2884623;
Flavell A.J., Dyson J., Ish-Horowicz D.;
"A novel GC-rich dispersed repeat sequence in Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asymmetric dimethylarginine
                                                                                        Bystematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gly/DMA-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BT001738; AAN71493.1; -.
EMBL; X05285; CAA28903.1; ALT_FRAME.
HSSP; 057811; 1G8A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase, FBgn0003062, Fib.
InterPro, IPR000692, Fibrillarin.
Pfam, PF01269, Fibrillarin, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE003459; AAF46950.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IntAct; Q9W1V3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rRNA processing.

DOMAIN

9
MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
                                                                                                                                                                                                                                                                                                                               melanogaster."
                                                             Lewis S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22426072; PubMed=12537575;
MEDLINE=22426072; PubMed=12537575;
Bergman C.M., Pfeiffer B.D., Rincon-Limas D.E., Hoskins R.A.,
Gnirke A., Mungall C.J., Wang A.M., Kronmiller B., Pacleb J.M.,
Park S., Stapleton M., Wan K.H., George R.A., de Jong P.J., Botas J.,
Rubin G.M., Celniker S.E.;
Rubin G.M., Celniker S.E.;
Rubin G.M., Celniker S.E.;
Genome Biol. 3.RESEARCHOBE.1-RESEARCHOBE.20(2002).
--- FUNCTION: Fibrillarin is a component of a nucleolar small nuclear ribonucleoprotein particle thought to participate in the first step in processing pretichosomal RNA. It is associated with the U3, U8 and U13 small nuclear RNAs (By similarity).
--- SUBCELLULAR LOCATION: Nuclear; fibrillar region of the nucleolus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 decededederrer decededede de restande de reconstructurantes de constructurantes de 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGGGGGGG----GGGGGGGGGGGGGGREKKRRQRRRGGGG------GGGGGGGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels 16; Gaps
                                               (Probable).
(Probable).
(Probable).
(Probable).
(Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: By homology to other fibrillarins, some or all of the N-terminal domain arginines are modified to asymmetric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 344;
       Asymmetric dimethylarginine (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dimethylarginine (DMA) (By similarity).
-!- SIMILARITY: Belongs to the fibrillarin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 199; DB 1;
Pred. No. 4.2e-09;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q811F4;
25-JAN-2005 (Rel. 46, Created)
25-JAN-2005 (Rel. 46, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBG10064623; Dere\Fib.
InterPro; IPR000662; Fibrillarin.
Pfan FF01269; Fibrillarin; I.
PRINTS; PR00052; FIBRILIARIN.
63
71
77
77
77
77
77
83
88
93
93
67
67
134
81
134
78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AY190941; AA001021.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila erecta (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                      66.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (By similarity).
           63
71
77
77
83
88
98
98
98
134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O57811; 1G8A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 GGG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 996 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fibrillarin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DROER
                                                                                                                                                                                                                                       MOD_RES
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Fib;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                               MOD_RES
MOD_RES
                                                                                           RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
FBRL DROER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FBRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
               8244444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
```

RNA-binding;	rginine (By		irginine (Probable). Irginine (Probable).	_	_		rginine (Probable).		-	Length 345; Indels 16; Gaps 3;		RGGRGGFGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		•					
ProDom; PD004637; Fibrillarin; 1. PROSITE; PS00566; FIBRILLARIN; 1. Methylation; Nuclear protein; Ribonucleoprotein; RNA-binding; FRNA processing. 9 109 Gly/DMA-rich.	Asymmetric dimethylarginine similarity).		Asymmetric dimetnylarginine Asymmetric dimethylarginine		-			Asymmetric dimethylarginine		Score 199; DB 1; 1 Pred. No. 4.3e-09; 1; Mismatches 5;	-GGGGGGGGGGGRKKRRQRRRGGGG-	GGGGGGGGFRGRGGGGGGGGGGGGGGGGGRGRGGGGGDRGGRGGFGGGGGGGGGG							
ProDom, PD004637; Fibrillarin, PROSITE, PS00566; FIBRILLARIN, Methylation, Nuclear protein; FRNA processing.		23 23	25 25	41 41	43 43	49 49		54 64 64					94	AA; 34709	66.8%; ilarity 65.1%; Conservative	99999999999999999999999999999999999999	GGGGGFRGRGGGGG	G 51 	ر 17 ام
	MOD_RES	MOD_RES	MOD_RES	MOD_RES	MOD_RES	MOD_RES	MOD_RES		£	MOD_RES	MOD_RES	MOD_RES	MOD KES	ENCE	Query Match Best Local Similarity Matches 41; Conser	1. 99.	13	49 GGG	555 69 111
TX X Y Y	FT	FT	FT	FT	ŦŦ	FT	FT	1 2	FT	FT	FT	F	. i	SS		ò	a	à	පි

Search completed: September 7, 2005, 12:59:58 Job time : 113.5 secs

This Page Blank (uspic)

OM protein - protein search, using sw model

Run on:

September 7, 2005, 12:44:44 ; Search time 65.5 Seconds
(without alignments)
301.142 Million cell updates/sec

US-09-910-432-19 Title:

Perfect score:

Sequence:

51

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

2105692

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

•• Database

A\_Geneseq\_16Dec04:\* 1: geneseqp1980s:\*

geneseqT1990s:\* geneseqT2000s:\* geneseqT2002s:\* geneseqT2002s:\* geneseqT2003ss:\* geneseqT2003bs:\* geneseqT2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Adc65108 HIV-TAT p	Adc65109 HIV-TAT p	Adc87061 Human GPC		Adj84541 T2R G-pro		Abg71303 PINPOINT	Abp29010 Streptoco		Abu22369 Protein e	Abo59421 Human gen		Abb64729 Drosophil	Aag51723 Arabidops		Adk14010 Chicken m	Ade77159 Human pro	۳	Abb36017 Peptide #	Aam29514 Peptide #		Abb21422 Protein #	Aam69190 Human bon	Human	Abg50867 Human liv
ΙD	ADC65108	ADC65109	ADC87061	ADG88556	ADJ84541	ADM96215	ABG71303	ABP29010	ABB60010	ABU22369	AB059421	ABU40120	ABB64729	AAG51723	ADH22061	ADK14010	ADE77159	AAM17023	ABB36017	AAM29514	ABB30839	ABB21422	AAM69190	AAM56810	ABG50867
82	7	7	7	7	œ	œ	ß	ß	4	9	œ	9	4	٣	7	œ	œ	4	4	4	4	4	4	4	4
% Query Match Length DB	51	51	920	200	200	200	201	26	399	188	208	237	344	258	38	345	462	283	283	283	283	283	283	283	283
% Query Match	100.0	93.0	77.3	77.0	77.0	77.0	77.0	70.6	69.3	68.1	9.99	66.3	66.1	64.8	64.6	64.1	63.6	63.4	63.4	63.4	63.4	63.4	63.4	63.4	63.4
Score	298	277	230.5	229.5	229.5	229.5	229.5	210.5	206.5	203	198.5	197.5	197	193	192.5	191	189.5	189	189	189	189	189	189	189	189
Result No.	п	8	e	4	ι.	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

The invention relates to the induction or stimulation of hair growth. The method of the invention comprises the administration of vascular

Disclosure, Page 14; 47pp; English.

Aam04731 Peptide # Abg38794 Human pep Abb69751 Drosophil	Abb65751 Drosophil Adc08281 Rice prot Abb60364 Drosophil	Abg95083 Human tra Abg95084 Human tra Adr14649 Human NF-	Human		Ads88302 Human pro Aag79360 OsGRP-Al. Abr56404 Peptide l	Abr44505 Peptide 1 Aam16105 Peptide # Abh35090 Dentide #	
AAM04731 ABG38794 ABB69751	ABB65751 ADC08281 ABB60364	ABG95083 ABG95084 ADR14649	AAM78355 ABG95081	ADI26117 ABM81732	ADS88302 AAG79360 ABR56404	ABR44505 AAM16105 ABB25000	AAM28596
4 U 4	4 1 4	സമ	4 r	0000	യവയ	9 4 4	4
283 283 74	98 162 237	462 525 525	526 526	526 526	162 41	357	357
63.4 63.4	62.9	62.6	62.6	62.6	62.6 62.4 62.2	62.2	61.7
189 189 188.5	188.5 187.5 187.5	186.5 186.5	186.5	186.5	186.5 186 185.5	185.5	184
26 27 28	30 30 31	3 8 8 2 8 4	32 36	38	8 4 4 9 0 1	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	45

## ALIGNMENTS

```
Inducing or stimulating new hair growth and preventing hair regression comprises administration of vascular endothelial growth factor and its receptor agonist with a positively charged backbone with attached
                                                                                                                                                                                                         1. .20 \ensuremath{//}/ /note= "this region may consist of between 0-20 Gly \ensuremath{/}
                                                                                                                                                                                                                                          Misc-difference 32. .51 /note= "this region may consist of between 0-20 Gly
                                                                                                            Hair; growth; regression; follicle; restore; cosmetic; clinical; alopecia; injury; surgical trauma; burn; skin transplant; ulcer; chemotherapy; HIV-TAT.
                                                                                                                                                                                             Location/Qualifiers
                      ADC65108 standard; peptide; 51 AA.
                                                                                                                                                                                                                                                                                                                                                                                    (ESSE-) ESSENTIA BIOSYSTEMS INC.
                                                                                                                                                                      Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                      21-FEB-2003; 2003WO-US005564.
                                                                                                                                                                                                                                                                                                                                                             21-FEB-2002; 2002US-0359400P.
                                                                    (first entry)
                                                                                                                                                                                                                                                                  residues"
                                                                                                                                                                                                                                 residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-845018/78.
                                                                                          HIV-TAT peptide #1.
                                                                                                                                                                                                         Misc-difference 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          efficiency groups.
                                                                                                                                                                                                                                                                                                                                                                                                          Waugh J, Dake M;
                                                                                                                                                                                                                                                                                         WO2003072049-A2.
                                                                   18-DEC-2003
                                                                                                                                                                                                                                                                                                                 04-SEP-2003.
                                                                                                                                                             Synthetic.
                                             ADC65108;
RESULT 1
             ADC65108
```

contestal growth factor (VEGF), a VEGF receptor agonist, a producy form cor its salt form in a non covalent association complex with positively charged backbone having a plurality of attached efficiency groups. The positively-charged back bone (preferably polylysine) comprises a polymer continuely-charged back bone (preferably polylysine) comprises a polymer formula (Gly) in (Arg) m and flAT domains or fragments. The positively-charged backbone having a plurality of efficiency groups of 15000-130000 MW conferably with a polylysine backbone having a plurality of attached Gly prevides stimulation of new hair growth, increase in hair growth or prevention of hair regressing the hair growth, increase in hair growth or prevention of hair regressing the hair follicles. The composition is also useful for restorative purposes, increasing the number of hair follicles and the regrowth of hair follicles. The composition is also useful for restorative purposes and papropriate for use in any situation where there is a need or desire of appropriate for use in any situation where there is a need or desire of any growth such as alopedia, accidental injury, damage to hair follicle, inclainal wound, desire to modify physical appearance, inclainal wound, donor site wound from skin wound from skin transplant, unce or radiation of chemotherapy site in mammals such as monkeys cats, cows, dogs, gerbils, goats, guinea pigs, hamsters, horses, mice, prairie dogs, can be easily applied and enhances gloss, glow, brilliance, fullness, can be easily applied and enhances gloss, glow, brilliance, fullness, length, uster, patina, sheen, shine, thickness and volume are improved. Controlled-release matrix formulation delivers the composition over a 24 (preferably 8) hours period and the matrix is not readily washed off or that acts as the positively charged backbone in a composition of the 

Sequence 51 AA;

ö Gaps ö 100.0%; Score 298; DB 7; Length 51; 100.0%; Pred. No. 3.9e-21; 0; Indels 0; Mismatches 51; Conservative Best Local Similarity Query Match Matches ઠ

윱

ADC65109 standard; peptide; 51 AA ADC65109; 

(first entry) 18-DEC-2003

HIV-TAT peptide #2.

Hair; growth; regression; follicle; restore; cosmetic; clinical;
alopecia; injury; surgical trauma; burn; skin transplant; ulcer;
chemotherapy; HIV-TAT.

Human immunodeficiency virus 1. Synthetic

1. .20 /note= "this region may consist of between 0-20 Gly Location/Qualifiers Misc-difference

residues" residues"

WO2003072049-A2.

04-SEP-2003.

21-FEB-2003; 2003WO-US005564.

21-FEB-2002; 2002US-0359400P.

```
The invention relates to the induction or stimulation of hair growth. The method of the invention comprises the administration of vascular endothelial growth factor (VEGF), a VEGF receptor agoniat, a producing form or its salt form in a non covalent association complex with positively charged backbone having a plurality of attached efficiency groups. The positively-charged back bone (preferably polylysine) comprises a polymer charing positively-charged branching groups. The efficiency group is of formula (Gly) n (Arg) m and TAT domains or fragments. The positively-charged backbone has a plurality of efficiency groups of 1500-30000 MW correctably with a polylysine backbone having a plurality of attached Gly 3 Arg 7 groups with 5-30 % degree of lysine saturation. The composition provides stimulation of new hair growth, increase in hair growth or prevention of hair regression by the retention in the number of existing increasing the number of hair follicle cross-sectional area, increasing the number of hair follicles and the regrowth of hair increasing the number of hair follicles and the regrowth of hair increasing the composition is also useful for restorative purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cosmeceutical or cosmetic purposes, clinical or prophylactic purposes and appropriate for use in any situation where there is a need or desire of hair growth such as alopecia, accidental injury, damage to hair follicle, surgical trauma, burn wound, desire to modify physical appearance, incisional wound, donor site wound from skin transplant, ulcer or radiation of chemotherapy site in mammals such as monkeys cats, cows, dogs, gerbils, goats, guinea pigs, hamsters, horses, mice, prairie dogs, rabbits, rats, sheep's, squirrels and especially humans. The composition and be assally applied and enhances gloss, glow, brilliance, fullness, length, luster, patina, sheen, shine, thickness and volume are improved. (Ontrolled-release matrix formulation delivers the composition over a 24 (preferably 8) hours period and the matrix is not readily washed off or removed with water. The current sequence represents a HIV-TAT fragment that acts as the positively charged backbone in a composition of the
                                                                                                                                                                                                     Inducing or stimulating new hair growth and preventing hair regression comprises administration of vascular endothelial growth factor and its receptor agonist with a positively charged backbone with attached
                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 14; 47pp; English.
                              (ESSE-) ESSENTIA BIOSYSTEMS INC.
                                                                                                                                               WPI; 2003-845018/78.
                                                                                                                                                                                                                                                                                              efficiency groups.
                                                                                        Dake M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention.
                                                                                     Waugh J,
```

Sequence 51 AA;

Gaps ô Length 51; 3; Indels 93.0%; Score 277; DB 7; 94.1%; Pred. No. 3.6e-19; ive 0; Mismatches 3 Cuery Match
Best Local Similarity 94.13,

ö

51 

> ઠ 셤

RESULT 3 ADC87061

ADC87061 standard; protein; 920 AA.

01-JAN-2004 (first entry)

ADC87061;

Human GPCR protein SEQ ID NO:1514.

human; GPCR; guanosine triphosphate-binding protein coupled receptor; gene therapy 

Homo sapiens.

EP1270724-A2.

ä

Gaps

6 51

protein

•

(NAAD-) (ADSC-)

```
The invention describes an isolated taste transduction G-protein coupled receptor (I) e.g., T2R which is expressed in a taste cell, comprises greater than 60% sequence identity to a fully defined sequence of 335 (SI), 333 (S2), 299 (S3), 310 (S4), 224 (SS), 77 (S6), 209 (S7), 266 (S8), 300 (S9), 300 (S10), 155 (S11), 173 (S12), 94 (S13), 115 (S44), 68 (S15), 126 (S16) and 180 (S17) amino acids as given in the specification.
                                                                                                                              The present invention relates to a method of identifying a compound that regulates angiogenesis via the modulation of contactin associated protei 3 (CASPR3). The method involves contacting the compound with a CASPR3 polypeptide and determining the functional effect of the compound upon the CASPR3 polypeptide. The CASPR3 nucleic acid and encoded protein is useful as a drug target for anti-angiogenic therapies. The invention is also useful in gene therapy. The present sequence is poly Gly flexible linker. This sequence is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated taste transduction G-protein coupled receptor e.g., T2R useful for identifying compound that modulates taste signaling in taste
              Methods for identifying compounds which regulate angiogenesis via modulation of contactin associated protein 3 (CASPR3) for the used in diagnosis and therapy of diseases related to angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             taste transduction; G-protein coupled receptor; T2R; taste signaling; CAMP level; cGMP level; IP3 level; Ca(2+) level; electrical activity; human; G-protein coupled receptor; receptor; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T2R G-protein coupled receptor related linker seg id 94.
                                                                                                                                                                                                                                                                                                                                                Score 229.5; DB 7;
Pred. No. 2.8e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mueller
                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 94; 121pp; English.
                                                                                             Disclosure; SEQ ID NO 14; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ryba N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ84541 standard; protein; 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-FEB-2003; 2003US-00364861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00393634
                                                                                                                                                                                                                                                                                                                                                  77.0%;
                                                                                                                                                                                                                                                                                                                                                                    80.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hoon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zuker CS, Adler JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-203221/19
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZUKER C S.
ADLER J E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUELLER K
                                                                                                                                                                                                                                                                                                             Sequence 200 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOON M.
RYBA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2004038312-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADJ84541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (RYBA/)
(MUEL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZUKE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ADLE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HOON/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cella
                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ84541
ID ADJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ï
                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The protein sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                       New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of guanosine triphosphate-binding protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Gly residues from position 6 to 200 may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 7; Length 920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          angiogenesis; contactin associated protein 3; CASPR3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
;
                                                                                                                                  NAT INST ADVANCED IND SCI & TECHNOLOGY.
CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 230.5; DB 7
Pred. No. 7.6e-14;
0; Mismatches 1
                                                                                                                                                                                           Suwa M, Asai K, Akiyama Y, Aburatani H;
                                                                                                                                                                                                                                                                                                                                                                      Claim 2; SEQ ID NO 1514; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADG88556 standard; protein; 200 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present or absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lorens JB, Xu W, Bogenberger J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 GGGGGGGGGGGGGGGGGGXG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 77.3%;
1 Similarity 80.4%;
41; Conservative 0
                                                     18-JUN-2002; 2002EP-00013517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAR-2002; 2002US-00100818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002US-00100818
                                                                                             18-JUN-2001; 2001JP-00246789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Poly Gly flexible linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RIGE-) RIGEL PHARM INC.
                                                                                                                                                                                                                                  WPI; 2003-315783/31.
                                                                                                                                                                                                                                                      N-PSDB; ADC87060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 920 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2003176333-A1
```

Query Match Best Local S

Matches

8 원 WPI; 2003-843828/78

18-MAR-2002;

18-SEP-2003

Unidentified

gene therapy

Human;

11-MAR-2004

ADG88556;

RESULT 4 ADG88556

```
in tage cells which involves contacting the compound with (I) and determining the functional effect of the compound (I). The functional cafeer is determined by measuring changes in intracellular CAMP, CAMP, CAMP, IP3, or Ca (2+). The functional effect is a chemical or physical effect. The functional effect is a chemical or physical effect. The functional effect is determined by measuring binding of the compound can extracellular domain of (I). The functional effect is determined by measuring binding of radiolabeled GTP to (I). (I) is recombinant and is from rat, mouse, or human. (I) is expressed in a cell or cell membrane. The functional effect is measured by determining changes in the electrical activity of cells (e.g., eukaryotic cell) expressing (I). (I) is useful for identifying compound that modulates taste signaling in taste cells which involves contacting a compound with (I). The extracellular domain (II) of (I) is useful for identifying a compound the compound with the polynucleotide encoding (I) and determining the functional effect of the compound upon the extracellular domain. This is the amino acid sequence of a T2R G-protein coupled receptor related
   is useful for identifying a compound that modulates taste signaling
```

## Sequence 200 AA;

```
ä
                   Gaps
                                   21
                                                   .,
6
8; Length 200;
                                   1; Indels
77.0%; Score 229.5; DB 8; 80.4%; Pred. No. 2.8e-14;
                 0; Mismatches
                  41; Conservative
        Local Similarity
Query Match
                  Matches
                                    δ
                                                    용
```

## RESULT

ADM96215 standard; protein; 200 AA

### ADM96215;

(first entry) 01-JUL-2004

## Poly Gly flexible linker.

G-protein coupled receptor 39; GPR 39; cancer; breast; ovary; prostate; brain; lung; ligand binding; aberrant receptor protein analysis; cytostatic; receptor; poly Gly flexible linker.

### Synthetic

Location/Qualifiers 6. .200 Misc-difference 6

/note= "Residues are independently optionally absent"

## US2004071708-A1

26-SEP-2002; 2002US-00255775

26-SEP-2002; 2002US-00255775

(IMMU-) IMMUSOL INC.

Claassen G, Li H, Barber J;

## WPI; 2004-373880/35

Identifying anticancer agents modulating G-protein coupled receptor proteins, comprises contacting GPR 39-specific binding agents to cancells and detecting anticancer activity to identify anticancer agent.

# Disclosure; SEQ ID NO 3; 33pp; English.

The invention relates to a method of identifying anticancer agents that modulate G-protein coupled receptor (GPR) proteins, comprising contacting

```
cept 39-specific binding agents to cancer cells and detecting anticancer activity. The invention also relates to a method of inhibiting cancer characteristics in cancer cells by down modulating GPR 39 protein.

Cativity to a level sufficient to inhibit the cancer characteristics of the cancer cells and an antibody that specifically recognises a GPR 39 protein. The method further involves binding a population of different compositions to the GPR 39 protein to select GPR 39-specific binding agents. The cancer cells are chosen from breast, ovarian, prostate, brain and lung cancer cells. The method is useful for identifying anticancer captures that modulate GPR 39 protein and for inhibiting cancer capture in cancer cells. The antibody is useful for inhibiting receptor function e.g. by blocking ligand binding, which is used in therapeutic function, in various in vitro histochemical techniques for detecting GPR proteins and as a diagnostic tool for aberrant receptor protein analysis. This sequence represents a poly Gly flexible linker used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting whether a first molecule is in close proximity to a second molecule, or detecting target molecule, by using a molecular beacon comprising an oligonucleotide to which a fluorophore and a quencher are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to detecting (M) whether a first molecule is in close proximity to a second molecule, or detecting a target molecule,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein position identification with nuclease tail; linker; PINPOINT; molecular beacon.
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         42
                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                               Score 229.5; DB 8; Length 200;
Pred. No. 2.8e-14;
0; Mismatches 1; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                       '. . .97
'note= "Optionally absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Optionally absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Col 59-60; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG71303 standard; protein; 201 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PINPOINT poly-Gly linker protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0080234P
                                                                                                                                                                                                                                                                                                                                     ch 77.0%;
1 Similarity 80.4%;
41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 105. .201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-749290/81.
                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 1
                                                                                                                                                                                                                                                                                                      Sequence 200 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-APR-1997;
03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US644441-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG71303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chung JH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         attached.
                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                         요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
```

7

cc involves using a molecular beacon that comprises an oligonuclectide (ON) to which a fluorophore and a quencher (FQ) are attached. The method is caped by brotein Position Identification with Nuclease Tail (FINDINT). The method further comprises, whether a first molecule is in close proximity to a second molecular beacon comprises an (ON) to which is rateched, and determining whether the first molecule is in close proximity to the second molecule by detecting whether fluorescence is cattached an (FQ), attaching an endonuclease (EN) moiety to the second molecule by detecting whether fluorescence is cantited by the fluorophore, where fluorescence mission is indicative of cleavage of the (ON) by the (EN) moiety, to cause separation of the (FQ). The method may also comprise, detecting a target molecule, which involves contacting the target molecule with a chimaeric fusion molecule that comprises an (EN) molecule and a quide molecule to the target molecule, contacting the chimaeric fusion molecule to the target comprises an (EN) molecule and a guide molecule to the target comprising an (ON) to which is attached a fluorophore and a quencher, and detecting the presence of a fluorescent signal which results from cleavage of the (ON) by the (EN), to allow separation of the quencher from the fluorophore. The method is useful for detecting interactions and concern in stru and in vitro, such as enzymatic reactions, hormonector in attu and in vitro, such as enzymatic reactions, hormonector in a proteinlinker used in the PINPOINT constructs of the invention ï Gaps DB 5; Length 201; 1; Indels Score 229.5; DB 5 Pred. No. 2.8e-14; 0; Mismatches 1 77.0%; 80.4%; Conservative Query Match Best Local Similarity Sequence 201 AA; 41; 

51 셤 ò

Streptococcus polypeptide SEQ ID NO 7196. ABP29010 standard; protein; 56 AA (first entry) 02-JUL-2002 ABP29010; RESULT 8

Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antinflammatory; infection; vaccine; meningitis; gene therapy.

Streptococcus agalactiae.

WO200234771-A2. 02-MAY-2002. 29-OCT-2001; 2001WO-GB004789

27-OCT-2000; 2000GB-00026333. 24-NOV-2000; 2000GB-00028727. 07-MAR-2001; 2001GB-00005640.

(CHIR-) CHIRON SPA. (GENO-) INST GENOMIC RES.

Fraser C; Grandi G, Margarit Y RosI, Masignani V, rettelin H; relford J,

WPI; 2002-352536/38. N-PSDB; ABN69641.

streptococcus/GBS (Streptococcus agalacties) or group A streptococcus/GBS (Streptococcus agalacties) or group A streptococcus gyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detect Streptococcus in a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to recombinantly produce (I) and may be streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying ä The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell such as meningitis, and for Gaps The invention relates to a protein (ABP25413-ABP30895) from group B Drosophila; developmental biology; cell signalling; insecticide; ٠. ف 21 Disclosure; SEQ ID NO 6822; 21pp + Sequence Listing; English Length 56; Indels Drosophila melanogaster polypeptide SEQ ID NO 6822. 4, 5, disease caused by Streptococcus bacteria, such detecting a compound that binds to the protein. Score 210.5; DB Pred. No. 6e-13; 0; Mismatches Myers EW; Claim 1; Page 3875; 4525pp; English. ABB60010 standard; protein; 399 AA PWD, 70.6%; 74.5%; 23-MAR-2001; 2001WO-US009231 23-MAR-2000; 2000US-0191637P 11-JUL-2000; 2000US-00614150 Query Match
Best Local Similarity 74.5' 26-MAR-2002 (first entry) Ŀ Drosophila melanogaster. Streptococcus proteins Venter JC, Adams M, WPI; 2001-656860/75. (PEKE ) PE CORP NY N-PSDB; ABL04113 Sequence 56 AA; WO200171042-A2. pharmaceutical. Interactions. 27-SEP-2001 ABB60010; RESULT 9 ABB60010 CCXSXLLLXSBXLXBXLXBXBXBXBXBXXXXXXXXXXCCC ð 셤

New Streptococcus protein for the treatment or prevention of infection or

```
ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                         GGGGGGGGCGCGGGGGGGGGGGGRFD-----RGGGGGGGRYDRGGGGGGGGGG
                                                                                                                                                                                                                                                            48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid compxising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense autisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense; prokaryotic essential gene; cell proliferation; drug design.
useful in developmental biology and in elucidating cell signalling and cell.cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaccutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                          Zyskind JW;
Xu HH;
                                                                                                                                                                                                                          17; Gaps
                                                                                                                                                                                         69.3%; Score 206.5; DB 4; Length 399; 68.9%; Pred. No. 6.7e-12;
                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein encoded by Prokaryotic essential gene #7896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     claim 25; SEQ ID NO 50293; 1766pp; English.
                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU22369 standard; protein; 188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-071-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0372851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAR-2002; 2002US-0362699P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                         Local Similarity 68.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-029926/02.
N-PSDB; ACA26239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burkholderia mallei
                                                                                                                                                        Sequence 399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                            270 G 270
                                                                                                                                                                                                                                                                                                                            49 G 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-OCT-2002
                                                                                                                                                                                                                                                                                           215
                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU22369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang
                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                           888888888888
                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                     용
                                                                                                                                                                                                                                                            ઠે
```

```
proliferation, (7) identifying a gene in an operon required to proliferation, (7) identifying a capound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; (9) manufacturing an antibiotic; (10) profiling a compound; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent of which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, content of the printed specification, but was obtained to the total form part of the printed specification, but was obtained to the content in the content of the printed specification, but was obtained to the print of the printed specification, but was obtained to the printed for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for surveying tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 GGGGGGGGGGGGDDGGYGGGGGGYGGGRDMERGGGGGRASGGGGAGARSGGGGGGGGG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Gaps
proliferation or the activity of a gene in an operon required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.1%; Score 203; DB 6; Length 18
68.9%; Pred. No. 7.9e-12;
ive 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome derived single exon protein #5655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABO59421 standard; protein; 208 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-APR-2002; 2002US-00029386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-APR-2002; 2002US-00029386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 68.9
hes 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-119264/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003194704-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 G 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 G 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABO59421
THE LANGE BY SERVE SERVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
```

```
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                             The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 mainto acids of any of the 6888 amino acids sequences fully defined in the specification. The probe is a single exon probe that expressed in human cells or tissues. Also included are a spatially.

CC expressed in human cells or tissues. Also included are a spatially.

addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a method of compriguous amino acids of any of the above- mentioned amino acid soft sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, acustomer desiring to measure gene expression, a method of sequences (optionally with conservative amino acid substitutions), and isolated antibody that binds specifically to a period cited above, acustomer desiring to measure gene expression a computer-readable construction data by subscription, and a computer-readable correct including data on the expression of a single exon probe cited above. The probes methods and apparatus are useful in gene correct measures to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising gross alternative splicing events, in detecting and characterising gross alternative splicing events, in detecting and characterising gross alternative splicing as in the expression are included are included. In addition, and reparations in priming the single exon microarra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USFTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 Geceserceseses resecencias de constantes de conseces de conseces de constantes de conseces de constantes de con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 8; Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein encoded by Prokaryotic essential gene #25647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seqdata.uspto.gov/sequence.html?DocID=20030194704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.6%; Score 198.5; DB 872.5%; Pred. No. 2.2e-11; ive 0; Mismatches 5
                          Claim 45; SEQ ID NO 33055; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU40120 standard; protein; 237 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 72.5
les 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU40120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU40120
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
```

```
the inventor interacts of an interact acts computating any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a proniferation of a cell. Also included are:

(1) a vector comprising a pronicer operably linked to the nucleic acid

c encoding a polypeptide whose expression is inhibited by the antiense

c nucleic acid; (2) a host cell containing the vector; (3) an isolated

c nucleic acid; (2) a nost cell containing the vector; (3) an isolated

contisense nucleic acid; (4) an antibody capable of specifically binding

the polypeptide; (5) producing the polypeptide; (6) inhibited by the

cut proliferation or the activity of a gene in an operon required for

proliferation or the activity of a gene in an operon required for

c proliferation, (7) identifying a compound that influences the activity of

the gene product or that has an activity against a biological pathway

c proliferation, (7) identifying a compound that influence the biological

c pathway in which a proliferation-required gene or its gene product lies

c or a gene on which the test compound that inhibits proliferation of an

c organism acts; (9) manufacturing an antibiotic; (10) profiling a

c compound's activity; (11) a culture comprising strains in which the gene

c product is overexpressed or underexpressed; (12) determining the extent

c product is overexpressed or underexpressed; (12) determining the extent

c proliferation of an organism. The antisense nucleic acids are useful for

dentifying proteins or screening for homologous nucleic acids required

c for cellular proliferation or how prover and acids are useful for

dentifying proteins or for screening homologous nucleic acids required

c for cellular proliferation or how isolate candidate molecined and acids and acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                             Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>.</u>
ن
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 decededecencies ececedente -----decededecededes of 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.3%; Score 197.5; DB 6; Length 237; 70.6%; Pred. No. 3.1e-11; ive 0; Mismatches 6; Indels 9.
                                                                                                                                                                                             Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 20979.
                                                                                                                                                                                             Haselbeck R,
                                                                                                                                                                                                                                   Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID NO 68044; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB64729 standard; protein; 344 AA
                                                                                                                                                                                                     Malone C,
                                                                                                                                                                                                                                       Carr GJ,
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                 (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                 Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                   WPI; 2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
tes 36; Conserv
                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ACA43990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB64729;
                                                                                                                                                                                                 Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB64729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ********
```

```
99US-0127462P.
99US-0128234P.
99US-0128234P.
99US-0130077P.
99US-0130049P.
99US-0130449P.
99US-0131449P.
99US-0132484P.
99US-0132484P.
                                                                                                                                                               99015 - 01324879

99015 - 01324879

99015 - 01342186

99015 - 01342187

99016 - 01342197

99016 - 01342197

99016 - 013431709

99016 - 01351247

99015 - 01351247

99015 - 01351247

99015 - 01351247

99015 - 01360219

99016 - 01375228

99016 - 01375228

99016 - 01375228

99016 - 01375228

99016 - 01375287

99016 - 01375287

99016 - 01394587

99016 - 01394587

99016 - 01394587

99016 - 01394587

99016 - 01394587

99016 - 01394587

99016 - 01394587

99016 - 01394628

99017 - 01394628

99018 - 01394628

99018 - 01394628

99018 - 01394628

99018 - 01394628

99018 - 01394628

99018 - 01394628

99018 - 01394628

99018 - 01394628

99018 - 01394628

99018 - 01394628

99018 - 01394628

99018 - 01394628

99018 - 01406328

99018 - 01406928

99018 - 01420548

99018 - 01420548

99018 - 01420548

99018 - 01420548

99018 - 01420548
                                                     19-AR-1999;
21-AR-1999;
23-ARR-1999;
23-ARR-1999;
30-ARR-1999;
30-ARR-1999;
04-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
21-JUN-1999;
22-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                             07-JUN-1999;
08-JUN-1999;
10-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                           10-JUN-1999;
14-JUN-1999;
16-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                          16-JUN-1999;
17-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUN-1999;
29-JUN-1999;
30-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JUL-1999;
16-JUL-1999;
                                                                                                                                                                                                                                                                                              25-MAY-1999
                                                                                                                                                                                                                                                                                                                              01-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUN-1999
  ij
                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABLi6176-ABL30511), expressed DNA sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                            4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 20979; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                     66.1%; Score 197; DB 4; Length 344; larity 70.9%; Pred. No. 4.6e-11; Conservative 0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 65674.
                                                                                                                                          Myers EW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG51723 standard; protein; 258 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0121825P.
99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126264P.
                                                                                                                                        Li PWD,
                                                                                  23-MAR-2000; 2000US-0191637P-
11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-2000; 2000EP-00301439
                                                               23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-OCT-2000 (first entry)
 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                        Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana.
                                                                                                                                                               WPI; 2001-656860/75.
                                                                                                                    (PEKE ) PE CORP NY.
                                                                                                                                                                          N-PSDB; ABL08832
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 344 AA;
                     WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1033405-A2
                                          27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG51723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG51723

110 AAG5

AC AAG5

XXX

XXX

XXX

XXX

XXX

DDB Arat

XXX

XXX

CET

PP EP 10

PP 25-F

PP 25-F

PP 25-F

PP 25-F

PP 25-F

PP 25-F
셤
```

1

```
990S-0144325P.
990S-0144331P.
990S-0144331P.
990S-0144333P.
990S-0144334P.
990S-0144334P.
990S-0144334P.
990S-0144334P.
990S-014508P.
990S-014688P.
990S-014932P.
990S-014934P.
                                                                                                                                                                                                                                                                                                                                                                                                           99US-0154039P.
99US-0154779P.
99US-0155139P.
99US-0155486P.
                                                                                                                                                                                                                                                                                                                                                                                                                                     9908-0155659P
9908-0156458P
9908-0157117P
9908-015753P
9908-015753P
9908-0158029P
19-70L-1999;
19-70L-1999;
19-70L-1999;
19-70L-1999;
19-70L-1999;
20-70L-1999;
20-70L-1999;
21-70L-1999;
21-70L-1999;
22-70L-1999;
22-70L-1999;
22-70L-1999;
23-70L-1999;
23-70L-1999;
23-70L-1999;
23-70L-1999;
23-70L-1999;
                                                                                                                                             27-JUL-1999)
28-JUL-1999)
02-AUG-1999)
02-AUG-1999)
03-AUG-1999)
04-AUG-1999)
05-AUG-1999)
05-AUG-1999)
06-AUG-1999)
06-AUG-1999)
06-AUG-1999)
                                                                                                                                                                                                                                                           13-AUG-1999;
13-AUG-1999;
16-AUG-1999;
17-AUG-1999;
18-AUG-1999;
20-AUG-1999;
                                                                                                                                                                                                                                                                                                        20-AUG-1999;
23-AUG-1999;
23-AUG-1999;
25-AUG-1999;
27-AUG-1999;
27-AUG-1999;
                                                                                                                                                                                                                                               11-AUG-1999
```

```
------GGGGGGGGGGGGVGDGYGYGRGWGGGYG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusion protein; human serum albumin; HSA; therapeutic protein; shelf-life; in vitro biological activity; in vivo biological activity; metabolic disorder; endocrine disorder; diabetes; type 1; type 2; diabetes-related condition; hyperglycaemia; neural disorder; neuropathy; retinopathy; cardiovascular disorder; heart disease; renal disorder; obesity; glucose level maintenance; weight loss; antidiabetic; cardiant; anorectic; ophthalmological; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic linker peptide, SEQ ID NO:858, inserted into proinsulin.
                                                                                                                                                                                                                                                                                                                                                                                Length 258;
                                                                                                                                                                                                                                                                                                                                                                            / Match 64.8%; Score 193; DB 3; Length 25 Local Similarity 57.6%; Pred. No. 8.6e-11; Nes 38; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADH22061 standard; peptide; 38 AA.
         9905-0159294P
9905-0159294P
9905-0159330P
9905-01593310P
9905-0159631P
9905-0159631P
9905-0160767P
9905-0160767P
9905-0160767P
9905-0160767P
9905-0160981P
9905-0160981P
9905-0160981P
9905-0160981P
9905-0160981P
9905-0161960P
                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 ¢ċċĠĠĠĠĠĠĠĠĠĠĠĠSĠPĠĠĠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-DEC-2001; 2001US-0341811P.
24-JAN-2002; 2002US-0350358P.
26-FEB-2002; 2002US-0359370P.
28-FEB-2002; 2002US-0360000P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-2002; 2002WO-US040892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 ĠĠĠĠĠ 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003059934-A2.
          13-OCT-1999)
13-OCT-1999)
14-OCT-1999)
14-OCT-1999)
14-OCT-1999)
14-OCT-1999)
14-OCT-1999)
12-OCT-1999)
12-OCT-1999)
13-OCT-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADH22061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46
                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADH22061
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                    용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

2

```
The invention relates to fusion proteins comprising human serum albumin (ADH21530) and a therapeutic polypeptide such as a therapeutic protein, antibody or peptide or their variants or fragments. The therapeutic protein may be fused to the N-terminus, the C-terminus or both termini of protein may be fused to the N-terminus, the C-terminus or both termini of albumin via a linker. The albumin component of the fusion proteins compared with those of the corresponding therapeutic proteins compared with those of the corresponding therapeutic proteins on their own. The invention also relates to nucleic acids concoling albumin fusion protein, vectors and host cells comprising an albumin fusion protein, the method of extending the shelf-life of a local plumin fusion protein with albumin, and the treatment of disease using an albumin fusion protein with albumin, and the treatment of disease conditions. Specifically the albumin fusion proteins may be used in the treatment of metabolic/endocrine disorders, diabetes and diabetes. The treat type I and type 2 diabetes, hyperglycaemia, neural disorders consisting the albumin fusion proteins may be used in the method of maintaining a basal glucose level in a method for losing weight. The present sequence is related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                   New albumin fusion protein, useful for preparing a composition for treating diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 24; SEQ ID NO 858; 1086pp; English.
                                   10-MAY-2002; 2002US-0378920; 24-JUL-2002; 2002US-037898008P. 09-AVG-2002; 2002US-0402131P. 13-AVG-2002; 2002US-0402131P. 18-SEP-2002; 2002US-0411355P. 02-OCT-2002; 2002US-0411355P. 11-OCT-2002; 2002US-0414984P. 23-OCT-2002; 2002US-0414984P.
                                                                                                                                                                                                               05-NOV-2002; 2002US-0423623P.
                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                               Rosen CA, Haseltine WA;
                                                                                                                                                                                                                                                                                                                                           WPI; 2003-598501/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 38 AA;
```

Gaps Query Match
64.6%; Score 192.5; DB 7; Length 38;
Best Local Similarity 74.5%; Pred. No. 2.1e-11;
Matches 35; Conservative 0; Mismatches 1; Indels 11; Н ઠ 셤

Search completed: September 7, 2005, 12:56:07 Job time : 68.5 secs

```
Sequence 13, Appli
Sequence 1, Appli
Sequence 40, Appli
Sequence 22, Appli
Sequence 6, Appli
Sequence 5, Appli
Sequence 112, Appl
Sequence 324, Appli
Sequence 1080, Appli
Sequence 1080, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1080, Apple Sequence 4, Appli Sequence 12, Appli Sequence 3, Appli Sequence 9, Appli Sequence 9, Appli Sequence 2, Appli Sequence 11006, A Sequence 1106, A Sequence 7, Appli Sequence 7, Appli Sequence 17, Appli Ap
                                                                                                                                              September 7, 2005, 12:48:54; Search time 29.5 Seconds (without alignments) 129.054 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                         51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                               Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-989-981A-13
US-09-05-995-1
US-09-053-003-40
US-09-054-281-25
US-09-18-094-40
US-09-18-094-40
US-09-65-013-112
US-09-65-013-112
US-09-575-574-4
US-09-17-34-9
US-09-157-34-9
US-09-157-34-137
US-09-137-4787
US-09-107-433-4573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                     513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
                                                                                                                                                                                                                                                  Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
```

28 168.5 56.5 420 2 US-08-845-998-8 Sequen 31 167 56.5 420 3 US-09-26-537-8 Sequen 32 168.5 56.5 420 3 US-09-280-837-8 Sequen 32 164 55.0 647 2 US-09-770-761A-8 Sequen 34 165.5 54.9 91 4 US-09-520-67-39789 Sequen 35 164 55.0 647 2 US-08-770-761A-8 Sequen 36 163.5 54.9 91 4 US-09-270-67-5506 Sequen 36 163.5 54.9 91 4 US-09-270-67-5506 Sequen 37 161 54.0 991 4 US-09-270-67-5506 Sequen 37 161 54.0 991 4 US-09-520-67-5506 Sequen 37 161 54.0 991 4 US-09-520-67-5506 Sequen 37 161 54.0 991 4 US-09-520-67-6623 Sequen 39 159.5 53.5 637 4 US-09-58-09-98-016-815 Sequen 41 159 53.4 300 3 US-08-756-56-3 Sequen 41 159 53.4 300 3 US-08-756-56-3 Sequen 41 159 53.4 300 3 US-08-756-56-3 Sequen 41 159 53.4 300 3 US-08-756-96-3 Sequen 42 159 53.4 300 3 US-08-756-96-3 Sequen 44 158.5 53.2 235 2 US-08-529-190B-1 Sequen 45 158.5 53.2 235 2 US-08-529-190B-1 Sequence 13, Application US/099991A Septican Trian, Hui Application US/099991A Septican Trian, Hui	ns 6-200 may be present of the control of the contr	66666666          6666666	
120 2 3 120 3 3 120 3 3 120 3 3 120 3 3 120 3 3 1 4 4 9 9 1 4 4 9 9 1 4 4 9 9 1 4 4 9 9 1 4 4 9 9 1 4 4 9 9 1 4 4 9 9 1 4 4 9 9 1 4 4 9 9 1 4 4 9 9 1 4 4 9 9 1 4 9 9 1 4 9 9 1 4 9 9 1 4 9 9 9 1 4 9 9 9 1 4 9 9 9 1 4 9 9 9 1 4 9 9 9 9	sitions Score Pred.	GGRGRDD	52995 ram ra A.
адашль и лошишичи — В В Ябббі∑і∑ийойоч∙ — О О		99999999999999999999999999999999999999	n US/090529 a, Mohanram ici, Berta Osvaldo A.
28 168.5 56.5 420 2 29 168.5 56.5 420 3 31 168.5 56.5 420 3 31 167 56.0 416 4 32 164 55.0 647 5 34 163.5 54.9 91 4 35 163.5 54.9 91 4 36 163.5 54.9 91 4 37 161 55.0 705 2 40 159 53.4 900 3 41 159 53.4 300 3 42 159 53.4 300 3 42 159 53.4 300 3 42 159 53.4 302 3 43 159 53.4 302 3 44 158.5 53.2 235 2 8ULT 1 509-8981A-13 5040ENCH 1500ENCH APPLICANT: BARNEW, Belen H. APPLICANT: BARNEW, RODERT APPLICANT: BARNEW, RODER: US OF ELICANT: BARNEW, BOATC OF ENCHORMER: US OF ELICANT: BARNEW, BOATC OF ENCHORMER: US OF ELICANT: BOATC OF ELICANT: BOATC OF ELICANT: BOATC OF ENCHORMER: US OF ELICANT: BOATC OF ELICANT: COOL-11-20 TYPE: PRIOR APPLICATION NUMBER: US OF ELICANT: APPLICATION NUMBER: US OF ELICANT: COOL-11-20 TYPE: PRIOR APPLICATION NUMBER: US OF ENCHORMER: US OF ENCHORMER: US OF ENCHORMER:	(20C TION: larity Conser	GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	pplication 83956 RMATION: Sivaraj Strulov Flores,
		, H H	JT 2 9-052-995-1 plence 1, Agreen No. 616 ENERAL INFOR APPLICANT: APPLICANT:
28 168 29 168 30 168 31 163 32 11 32 11 33 163 34 163 35 163 36 163 39 159 40 11 42 11 42 11 42 11 44 1158 45 159 45 159 46 11 47 158 48 158 4	; LOCATI ; OTHER US-09-989- Query Ma Best Loc Matches	qo Qo	RESULT 2 US-09-052-995-1 Sequence 1, A Patent No. 61 GENERAL INPO APPLICANT: APPLICANT: APPLICANT:

```
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 22:
                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Modified-site
                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 105..201
OTHER INFORMATION: /
OTHER INFORMATION: /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-053-003-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-09-054-281-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ଚ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
TITLE OF INVENTION: High Throughput In Vitro Screening Assay
TITLE OF INVENTION: for Transcription Modulators
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DE-DOS/MS-DOS
OFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/09/652,995
FILING DATE: 31-MAR-1996
CLASSIFICATION NUMBER: US/09/652,995
FILING DATE: 31-MAR-1996
CLASSIFICATION NUMBER: US/09/652,995
FILING DATE: 31-MAR-1996
CLASSIFICATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 018781-000600US
TELECOMMUNICATION INFORMATION:
TELEFRAX: (415) 576-0300
INPORMATION POR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FUNCTURENT CHARACTERISTICS:
FUNCENT TABLEFAX: CALASTERISTICS:
FUNCTURENT CHARACTERISTICS:
FUNCENTER TRANSIES OF CALASTERISTICS:
FUNCENT TABLEFAX: CALASTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 40, Application US/09053003
Fatent No. 6207391
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wu, Pengquang
APPLICANT: Wckinney, Judi
TITLE OF INVENTION: High-Throughput Screening Assays for
TITLE OF INVENTION: Modulators of STAT4 and STAT6 Activity
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STAEET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.0%; Score 229.5; DB 3; Length 201; 80.4%; Pred. No. 3.8e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/053,003
FILING DATE: 31-MAR-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 201 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-053-003-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-052-995-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------GGGGGGGGGGGGGGGGGG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9;
                                                                                                                                                                                                                                                                                                                                  /product= "OTHER"
/note= "Gly at positions 105-201 may be
present or absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 201;
                                                                                                                                                                                                 NAME/KEY: Modified-site
LOCATION: 1..97
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /present or absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/054,281
FILING DATE: 02-APR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/080,234
FILING DATE: 03-APR-1997
FILING DATE: 03-APR-1997
ATTORNEY/AGENT INFORMATION:

NAME: SMITh, Timothy L.

REFERENCE/POCKET NUMBER: 015280-295200US
TELECOMMUNICATION NUMBER: 35,367
REFERENCE/POCKET NUMBER: 015280-295200US
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 77.0%; Score 229.5; DB 3; Best Local Similarity 80.4%; Pred. No. 3.8e-15; Matches 41; Conservative 0; Mismatches 1;
018781-000800US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111-3834
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
```

Ξ,

```
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                               ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09478948
; Retent No. 646528
; GRERAL INFORMATION:
; APPLICANT: Shan, Bei
; APPLICANT: CANT: CANDOLON:
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: Metabolism
; FILE REFERENCE: 018781-001310US
; CURRENT PILING DATE: 2000-01-06
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARR: PatentIN Ver. 2.1
; SEQ ID NO 6
; LENGTH 201
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:flexible linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MOD_RES
LOCATION: (1)..(97)
OCHER INFORMATION: Gly at positions 1-97 may be present or absent
NAME/KEY: MOD_RES
LOCATION: (105)..(201)
OTHER INFORMATION: Gly at positions 105-201 may be present or absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "OTHER"
/note= "Gly at positions 105-201 may be
present or absent"
                                                                                                                                                                                                                                                                                                                                                                                    77.0%; Score 229.5; DB 4; Length 201; ilarity 80.4%; Pred. No. 3.8e-15; Conservative 0; Mismatches 1; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 201;
                                                                                                                                                                       /product= "OTHER"
/note= "Gly at positions 1-97 may be
present or absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 77.0%; Score 229.5; DB 4; Length; Best Local Similarity 80.4%; Pred. No. 3.8e-15; Matches 41; Conservative 0; Mismatches 1; Indels
                  LENGTH: 201 amino acida
TYPE: amino acid
STRANDEDNESS:
TOPOLOCY: linear
MOLECULE TYPE: peptide
FRATURE:
NAME/KEY: Modified-site
LOCATION: 1..97
OTHER INFORMATION: /produc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                 Modified-site
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acid
                                                                                                                                                                                     OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
NAME/KEY: Modified-
                                                                                                                                                                                                                                                               LOCATION: 105..201
COTHER INFORMATION:
OTHER INFORMATION:
COTHER INFORMATION:
US-09-054-281-22
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 41; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                        41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-478-948-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
```

; Sequence 40, Application US/09818094 ; Patent No. 6682898

US-09-818-094-40

RESULT 6

```
Gaps
RAL INFORMATION.

APPLICANT: Wu, Pengguang
McKinney, Judi
TITLE OF INVENTION: High-Throughput Screening Assays for
Modulators of STAT4 and STAT6 Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.0%; Score 229.5; DB 4; Length 201; 80.4%; Pred. No. 3.8e-15; tive 0; Mismatches 1; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09754947
Sequence 10. 6828110
GENERAL INFORMATION:
APPLICANT: Lee, Burce Andrew
APPLICANT: Flores, Becky Mar
APPLICANT: Valkirs, Gunars Edwin
APPLICANT: Blosite Diagnostics, Inc.
TITLE OF INVENTION: Assays for Detection of Bacillus Anthracis
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NAMBER: US/09/818,094
FILING DATE: 26-Mar-2001
CLASSIFICATION: <Unknown>
                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew Life
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/053,003
FILING DATE: 31-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REFERENCE/DOCKET NUMBER: 35,367
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /notes "Gly at positions 105-201 may be present or absent" SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "OTHER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1..97
OTHER INFORMATION: /product= "OTHER
//note= "Gly at positions 1-97 may be
present or absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 201 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 105..201
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 80.4%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-818-094-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-754-947-5
```

```
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR PLING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PREL PROGram
SEQ ID NO 324
LENGTH: 462
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 GGGGGGGGUYGQDQSSMSSGGGSGGGYGNQDQSGGGSGGYGQQDRGRRGRGSGGGG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cy-vy-bs-vya-lioud

gequence 1080, Application US/09538092

gequence 1080, Application US/09538092

general No. 6753314

GENERAL INFORMATION:

APPLICANT: Glot, Loic

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

FILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-04-01

PRIOR PILING DATE: 2000-02-01

NUMBER: 60/178,965

PRIOR FILING DATE: 2000-02-01

NUMBER: CuraPatSeqFormatter Version 0.9

SEQ ID NO 1080

LENGUTH: 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 doddodddanydoddssmssaaasadayanoddsadaasadydodhaararaasadda 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GGG-----GGGGGGGRGRDDRRQRRRGGGGGG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (0). T. (0) OTHER INFORMATION: Polypeptide Accession Number P35637
                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 1813444CD1
US-09-919-039-324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 63.6%; Score 189.5; DB 4; Best Local Similarity 48.2%; Pred. No. 4.5e-11; Matches 41; Conservative 2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.6%; Score 186.5; DB 4;
48.2%; Pred. No. 9.6e-11;
iive 1; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 GGGGGYNRSSGGYEPRGRGGGRGG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 GGGGGGYNRSSGGYEPRGRGGGRGG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 GGGGG------GGGGGG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --- GGGGGG 50
  Application US/09919039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Homo sapiens FEATURE: NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGGGGGGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 GGGGGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-538-092-1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-538-092-1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: 20ghbi, Huda Y.
APPLICANT: 20ghbi, Huda Y.
APPLICANT: Van den Veyver, Ignatia B
APPLICANT: Van den Veyver, Ignatia B
APPLICANT: Amir, Ruthie
APPLICANT: Amir, Ruthie
APPLICANT: Amir, Ruthie
APPLICANT: Prancke, Uta
TITLE OF INVENTION: Wethods of Identifying Mutations in a Methyl-CPG-Binding Domain
TITLE OF INVENTION: Containing Gene or Protein in Neurodevelopmental Disease and Tre
FILE REFERENCE: HO-POLS93UG1/09905371
CURRENT APPLICATION NUMBER: US/09/657,013
CURRENT FILING DATE: 2000-09-07
PRIOR PILING DATE: 1999-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 GGGGGGGGGGGGGGRVGGGGGGRVRAABERGGGRLLVKMPFAGGGAPASPPAPPTPLP 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 PSAAHPPPTAPPATHGQGLGGGVKRPGRKRKAEADSRSVPKKRGRKPGGGGGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence:flexible linker NAME/KEY: MOD RES.
LOCATION: (1) - (97)
OTHER INFORMATION: Gly at positions 1-97 may be present or absent NAME/KEY: MOD RES.
LOCATION: (105) ... (201)
LOCATION: (105) ... (201)
CHER INFORMATION: Gly at positions 105-201 may be present or absent US-09-754-947-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 77.0%; Score 229.5; DB 4; Length 201; Similarity 80.4%; Pred. No. 3.8e-15; 41; Conservative 0; Mismatches 1; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 191; DB 4; Length 345;
Pred. No. 2.5e-11;
1; Mismatches 5; Indels '
              CURRENT APPLICATION NUMBER: US/09/754,947
CURRENT FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: US 60/174,901
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PARCHIIN Ver: 2.1
SEQ ID NO 5
LENGTH: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGGGGGGGGGGGG--GGGGRGR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 112, Application US/09657013; Patent No. 6709817
FILE REFERENCE: 014907-003310US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vuery march
Best Local Similarity 35.4%;
Matches 45; Conservative
                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin version 3.1
SEQ ID NO 112
LENGTH: 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGGVGG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGGGG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -09-657-013-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-657-013-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-09-919-039-324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
```

ઠે 셤 ઠે g 요 ò

ઠે

```
61.4%; Score 183; DB 4; Length 10
67.3%; Pred. No. 5.2e-11;
ive 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MALDIA HIST LIBER COMPUTER: OF COMPUTER: IN COMPUTER: OF 
Sequence 4, Application US/09411067C Patent No. 6576610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08864038A Patent No. 6001592 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Spacer element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212)986-2340
TELEFAX: (212)953-7733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: 812-5 Hirano
STREET: Isshinden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 61.49
Best Local Similarity 67.33
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212)953-7733
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Isshinden
CITY: Tsu-city
STATE: Mie-prefecture
COUNTRY: JAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               514-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-864-038A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                 100
                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/09832297A

Sequence 12, Application US/09832297A

Patent No. 6652836

GENERAL INFORMATION:
APPLICANT: Fluoroprobe, Inc.
APPLICANT: LUIKEN, George A.
TITLE OF INVENTION: METHOD FOR VIEWING TUMOR TISSUE LOCATED WITHIN A BODY CAVITY
FILE REFERENCE: FLUORI1120-2
CURRENT PELLING DATE: 2001-04-09
FRIOR APPLICATION NUMBER: US/09/832,297A
CURRENT FILING DATE: 1999-07-28
FRIOR APPLICATION NUMBER: US 09/362,805
FRIOR FILING DATE: 1998-10-15
NUMBER OF SEQ ID NOS: 12
SOFFWARE: PatentIn version 3.1
SEQ ID NO 12
LEMOTHER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (3)..(57)
; OTHER INFORMATION: Amino Acids at residues 3 to 7 could be repeated up to 10 times
US-09-832-297A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: REPEAT
LOCATION: (3)..(6)
OTHER INFORMATION: Amino Acid at residue 3 could be repeated up to 3 times
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.4%; Score 183; DB 4; Length 60;
67.3%; Pred. No. 3.4e-11;
tive 0; Mismatches 16; Indels
                                                          US-09-575-574-4
; Sequence 4, Application US/09575574
; Patent No. 6376750
; GENERAL INFORMATION:
; APPLICANT: Yu, Su-May
; APPLICANT: Chao, Yu-Chan
; TITLE OF INVENTION: PLANT SEEDLING AND EMBRYO PROMOTER
; TITLE REFERENCE: 08919-047001
; CURRENT FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.4%; Score 186; DB 3; 72.0%; Pred. No. 4e-11; tive 1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Peptide linker moiety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 62.4
Best Local Similarity 72.0
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: REPEAT
LOCATION: (3)..(9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-832-297A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-09-411-067C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-575-574-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
APPLICANT: NUVAS, LLC
APPLICANT: HOUSTON, L.L.
TITLE OF INVENTION: USE OF A CONTEXT-DEPENDENT FUNCTIONAL ENTITY TO ENHANCE THE EFFICY
TITLE OF INVENTION: AN AGENT
FILE REFERENCE: NUVASI140
CURRENT APPLICATION NUMBER: US/09/411,067C
CURRENT FILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: REPEAT
LOCATION: (1)..(5)
COTHER INFORMATION: Spacer peptide variation; sequence repeated "n" times, where n = US-09-411-067C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kunio NAKASHIMA et al.

TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR

TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID

TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING

TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY

TITLE OF INVENTION: TO SAID POLYPEPTIDE

NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 100
```

ä;

```
ö
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.1%; Score 182; DB 2; Length 268; 69.1%; Pred. No. 1.5e-10;
                                                                                                                                                                                                                                                                   Score 183; DB 3; Length 738;
Pred. No. 2.7e-10;
0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08835099A
Patent No. 5874277
GENERAL INFORMATION:
APPLICANT: SHINTANI, Yasushi
APPLICANT: KARAMOTO, Tomohiro
TITLE OF INVENTION: NOVEL PROTEINS, THEIR PRODUCTION
TITLE OF INVENTION: NOVEL PROTEINS, THEIR PRODUCTION
TITLE OF INVENTION: ADD USE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTY: USA
ZIF: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: DISKETE
COPERATING SYSTEM: DOS
SOFTWARE: FASESEG for Windows Version 2.0
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,099A
FILING DATE: 04-APR-1997
CLASSIFICATION NUMBER: 083649/1996
FILING DATE: 05-APR-1996
FILING DATE: 03-APR-1996
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Resenick, David S
REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
REGISTRATION INFORMATION:
NAME: Resenick, David S
REGISTRATION NUMBER: 34,235
TELECOMMUNICATION INFORMATION:
TELEPHONE: 61-523-3400
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORGANISM: Pinctada fucata
CELL TYPE: mantle epithelial cell
FEATURE:
NAME/KEY: peptide
LOCATION: from 1 to 738
JDBNITFICATION METHOD: E (by experiment)
US-08-864-038A-3
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 64.7%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      // MOLECULE TYPE: protein US-08-835-099A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-08-835-099A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: M
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

```
12; Gaps
                     ---Accececececececececece
5; Indels
0; Mismatches
                                          10 GGGGGGGGGLGGCLGNVLGGLISG
38; Conservative
Matches
                     à
                                          셤
```

Search completed: September 7, 2005, 13:01:57 Job time : 30.5 secs

Sequence 8, Ay Sequence 3, Ay Sequence 3, Ay Sequence 15, Sequence 13, Sequence 13,

8, Applii 3, Applii 3, Applii 15, Applii 25, Applii 26, Applii 27, Applii 27, Applii 27, Applii 28, Applii 30, Applii 31, Applii

Sequence Sequence Sequence Sequence

Scoring table:

Total number

Minimum I Maximum I

Searched:

Database :

Perfect score:

Sequence:

protein

Š

Run on:

Sequence Sequence Sequence Sequence Sequence

Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence

Sequence

Sequence

Sequence

Sequence

```
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (32)...(51)
OTHER INFORMATION: Gly at positions 32-51 may be present or absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence:positively OTHER INFORMATION: charged HIV-TAT fragment branching group OTHER INFORMATION: (efficiency group) attached to solid backbone PEATURE:
NAME/KEY: MOD RES
LOCATION: (1)...(20)
OTHER INFORMATION: Gly at positions 1-20 may be present or absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Waugh, Jacob
APPLICANT: Bake, Michael
APPLICANT: Bake, Michael
APPLICANT: Bakentia Biooystems, Inc.
TITLE OF INVENTION: Multi-Component Biological Transport Systems
FILE REFERENCE: 020154-0001100S
FILE REFERENCE: 020154-0001100S
CURRENT FILING DATE: 2001-07-20
PRIOR PLILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
US-10-026-331B-21

US-10-026-031-8

US-10-161-163-3

US-10-160-663-3

US-10-004-417-25

US-10-004-417-25

US-10-188-405-13

US-10-233-098-5

US-10-233-098-5

US-10-233-098-5

US-10-233-098-5

US-10-233-098-5

US-10-233-08-3

US-10-237-467-18

US-10-237-467-18

US-10-237-467-18

US-10-123-568-4

US-10-123-144-4

US-10-459-190-24

US-10-459-190-24

US-10-459-190-24

US-10-459-190-24

US-10-619-403-7

US-10-619-403-7

US-10-619-403-7

US-10-619-619-968-72

US-10-619-619-968-72

US-10-619-619-619-968-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19, Application US/09910432; Publication No. US20030229034A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
  US-09-910-432-19
  SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
    Sequence 19, Appl
Sequence 12, Appl
Sequence 1514, Ap
Sequence 18, Appl
Sequence 19, Appl
Sequence 18, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 24, Appl
                                                                                                               (without alignments)
352.368 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                  51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                7, 2005, 12:54:00 ; Search time 57 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
                                                                                                                                                                               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-910-432-19
US-09-910-432-20
US-09-910-432-20
US-00-798-584-19
US-09-98-667-19
US-09-998-667-18
US-09-998-667-18
US-09-990-940-21
US-09-990-940-21
US-09-990-940-21
US-09-990-940-21
US-09-990-940-21
US-09-980-381A-13
                                                                                                                                                                                                                                                                              of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                       1774312 seqs, 393823214 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      - protein search, using sw model
                                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                           DB seq length: 0
DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01166641111
                                                                                                                                                      US-09-910-432-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     September
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.3
77.0
77.0
77.0
77.0
77.0
```

US-09-910-432-19

229.5 229.5 229.5 229.5 229.5 229.5 229.5 229.5 229.5

4 7 7 10 10 11

Result

윰 ð

```
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MOD RES
LOCATION: (467)...(467)
                                                                        NAME/KEY: MOD_RES
                                                                                                                                                              NAME/KEY: MOD RES
LOCATION: (169)...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MOD RES
LOCATION: (295)...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MOD_RES
LOCATION: (350)...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MOD RES
LOCATION: (354)...
                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Geguence 1514, Application US/1029298

Sublication No. US2030235833A1

Publication No. US2030235833A1

Sublication No. US2030235833A1

Sublication No. US2030235833A1

Sublication No. US203023583A1

Subticant: SUMA, MAKIKO

APPLICANT: ABMIX KYYOSHI

APPLICANT: ARYAMA, YUTAKA

APPLICANT: ABMIX AUTAKA

TILLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS

FILE REFERENCE: 084335/166

CURRENT PAPLICATION NUMBER: 10/017,161

PRIOR FILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-66-18

NUMBER OF SEQ ID NOS: 2070

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1514
                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                   Gaps
                                                                                                                                                                                                                    US-09-910-432-20

Sequence 20, Application US/09910432

Sequence 20, Application US/09910432

Publication No. US20030229034A1

GENERAL INFORMATION:

APPLICANT: Waugh, Jacob

APPLICANT: Dake, Michael

APPLICANT: BESENTIA Biologytems, Inc.

TITLE OF INVENTION: Multi-Component Biological Transport Systems

FILE REPERENCE: 020154-000110US

CURRENT PILING DATE: 2001-07-20

PRIOR APPLICATION NUMBER: US/09/910,432

CURRENT FILING DATE: 2000-07-21

PRIOR PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRATURE:
NAME/KEY: MOD RES
LOCATION: (327..(51)
OTHER INFORMATION: Gly at positions 32-51 may be present or absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1)..(20)
OTHER INFORMATION: Gly at positions 1-20 may be present or absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence:positively OTHER INFORMATION: charged HIV-TAT fragment branching group OTHER INFORMATION: (efficiency group) attached to solid backbone
                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
    DB 10; Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
93.0%; Score 277; DB 10; Length 51;
Best Local Similarity 94.1%; Pred. No. 3.3e-16;
Matches 48; Conservative 0; Mismatches 3; Indels
                                            0; Indels
TYPE: PRT
ORGANISM: Artificial Sequence
                       Best Local Similarity
Matches 51; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)..(2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-292-798-1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-910-432-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 20
LENGTH: 51
  Query Match
```

ð 셤

```
NAME/KEY: MOD RES
LOCATION: (231)...(231)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MOD RES
LOCATION: (233)..(233)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MOD RES
LOCATION: (434)..(434)
OTHER INFORMATION: Variable amino acid
LOCATION: (119)..(166)
OTHER INFORMATION: Variable amino acid
                                                                                                      LOCATION: (169)..(186)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                    NAME/KEY: MOD RES
LOCATION: (188)..(188)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                 LOCATION: (215)...(215)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MOD RES
LOCATION: (265)...(265)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (289)..(289)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (295)...(295)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MOD RES
LOCATION: (302)...(303)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (316)..(316)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (321).. (321)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (345)..(345)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (354)..(354)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (429)..(429)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (350)..(350)
OTHER INFORMATION: Variable amino acid
```

```
FEATURE:
NAME/KEY: MOD RES
LOCATION: (485)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: MOD RES
LOCATION: (492)
O'THER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: MOD RES
LOCATION: (633)..(633)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MOD RES
LOCATION: (671)..(671)
OTHER INFORMATION: Variable amino acid
                                                                                             FEATURE:
NAME/KEY: MOD_RES
LOCATION: (479).
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MOD RES
LOCATION: (551)...(551)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MOD RES
LOCATION: (555)..(603)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAWE/KEY: MOD RES
LOCATION: (607)..(622)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WAME/KEY: MOD RES
COCATION: (624)..(625)
JTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MOD RES
LOCATION: (631)..(631)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WANE/KEY: MOD RES
LOCATION: (636)..(636)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MOD RES
LOCATION: (642)..(642)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ION: (645)..(645)
INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MOD RES
LOCATION: (651)..(651)
OTHER INFORMATION: Variable amino acid
OTHER INFORMATION: Variable amino acid
                                                        LOCATION: (469)..(469)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                              ION: (499)..(499)
INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (655).. (656)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (664)..(664)
OTHER_INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                  COCATION:
```

```
RESULT 4

US-09-798-584-18

i Sequence 18, Application US/09798584

j Patent No. US20020102676A1

j GENERAL INFORMATION:

APPLICANT: Mu, David

APPLICANT: POWETS, Scott

APPLICANT: PLIATE INC.

TITLE OF INVENTION: KORS: A No. US20020102676A1e1 Potassium Channel Protein

FILE REFERENCE: 018781-004010US

CURRENT APPLICATION NUMBER: US/09/798,584

CURRENT FILING DATE: 2001-03-03

PRIOR FILING DATE: 2000-03-03

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 18

LENGTH: 200

TYPE: APPLICATION OF THE NOS: 18

SEQ ID NO 18

TYPE: APPLICATION OF THE NOS: 18

SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:poly-Gly linker:
NAME/KEY: MOD RES:
COTION: (6)..(200)
OCHER INFORMATION: Gly at positions 6-200 may be present or absent
US-09-798-584-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 15; Length 920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 77.3%; Score 230.5; DB 15; Length Best Local Similarity 80.4%; Pred. No. 1.7e-11; Matches 41; Conservative 0; Mismatches 1; Indels
NAME/KEY: MOD RES
LOCATION: (676)..(676)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                 NAME/KEY: MOD RES
LOCATION: (698)...(699)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                        PERLACKEY: MOD RES
LOCATION: (715)..(715)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KRY: MOD RES
LOCATION: (723)..(723)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEX: MOD RES
LOCATION: (731)..(731)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                     NAME/KEY: MOD RES
LOCATION: (683)..(684)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (725)..(726)
OTHER INFORMATION: Variable amino acid
                                                                                         NAME/KEY: MOD RES
LOCATION: (678)..(678)
OTHER INFORMATION: Variable amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MOD_RES
LOCATION: (736)..(736)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
```

77.0%; Score 229.5; DB 9; Length 200;

Query Match

ï

Gaps

6

Length 200; Indels

요

ò

```
US-09-921-159-34

| Sequence 34, Application US/09921159
| Sequence 34, Application US/09921159
| Sequence 34, Application US/09921159
| Publication No. US20030017533A1
| GENERAL INFORMATION:
| APPLICANT: US-04, Unit Dickson
| APPLICANT: US-04, Unit Dickson
| APPLICANT: ICAgen, Inc.
| TITLE OF INVENTION: Slo2 and Slo4, Novel Potassium Channel Proteins from
| TITLE OF INVENTION: Human Brain
| FILE REPERRNCE: 018512-006810W
| CURRENT FILING DATE: 2002-01-17
| PRIOR APPLICATION NUMBER: US 60/249,112
| PRIOR FILING DATE: 2000-11-15
| NUMBER OF SEQ ID NOS: 38
| SOFTWARR: PatentIn Ver: 2.1
| SEQ ID NO 34
| LENGTH: 200
                          PEATURE:
OTHER INFORMATION: Description of Artificial Sequence:flexible linker:
OTHER INFORMATION: Description of Artificial Sequence:flexible linker:
NAME/KEY: MOD RES
LOCATION: (6) - (200)
OTHER INFORMATION: Gly at positions 6-200 may be present or absent US-09-998-667-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) LOCATION: (6) ... (200)
; OTHER INFORMATION: Gly at positions 6-200 may be present or absent
US-09-921-159-34
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 77.0%; Score 229.5; DB 10; Length 200; Best Local Similarity 80.4%; Pred. No. 6.7e-12; Matches 41; Conservative 0; Mismatches 1; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:poly Gly
OTHER INFORMATION: flexible linker
NAME/KEY: NOT RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gupte, Jamila S.
APPLICANT: Gupte, Jamila S.
APPLICANT: Tularik Inc.
TITLE OF INVENTION: No. US20030027252A1e1 Receptors
FILE REFERENCE: 018781-007410US
CURRENT APPLICATION NUMBER: US/09/990,940
CURRENT FILING DATE: 2001-11-21
                                                                                                                                                                                                                                     Match 77.0%; Score 229.5; DB 9; Local Similarity 80.4%; Pred. No. 6.7e-12; les 41; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21, Application US/09990940
Publication No. US20030027252A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao, Jiagang
Chen, Jin-Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cutler, Gene
An, Songzhu
Dai, Kang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tian, Hui
APPLICANT: Zhao, Jii
APPLICANT: Chen, Jii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-990-940-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                   ï
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (6)...(200)
OTHER INFORMATION: Gly residues from position 6 to 200 may be present
OTHER INFORMATION: or absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Masuda, Esteban
APPLICANT: Masuda, Esteban
APPLICANT: Liao, X. Charlene
APPLICANT: Liao, Haoran
APPLICANT: Chu, Haoran
APPLICANT: Chu, Peter
APPLICANT: Pardo, Jorge
APPLICANT: Rigel Pharmaceuticals, Incorporated
TITLE OF INVENTION: TRACI: Modulators of Lymphocyte Activation
FILE REFERENCE: 021044-006600US
CURRENT APPLICATION NUMBER: US/09/998,667
CURRENT FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: US 60/282,432
PRIOR PILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 18
SQFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 200
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence:poly Gly tag
OTHER INFORMATION: flexible linker
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pardo, Jorge
APPLICANT: Li, Congfen
APPLICANT: Li, Congfen
APPLICANT: Zhao, Haozan
APPLICANT: Aho, Haozan
APPLICANT: Rigel Pharmaceuticals, Inc.
TITLE OF INVENTION: PAZ: Modulators of Lymphocyte Activation
TITLE OF INVENTION OF PAZ: Modulators of Lymphocyte Activation
FILE REFERENCE: 021044-000700US
CURRENT APPLICATION NUMBER: US/09/967,624
PRIOR PILING DATE: 2001-09-28
PRIOR PILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver: 2.1
                                   6
                                                                                                                                 1 dedecedededededededededen -----dedecededededededed 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.0%; Score 229.5; DB 9; Length 200; 80.4%; Pred. No. 6.7e-12;
     80.4%; Pred. No. 6.7e-12;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                        Sequence 19, Application US/09967624
Patent No. US20020142325A1
GENERAL INFORMATION:
APPLICANT: Liao, X. Charlene
APPLICANT: Chu, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18, Application US/09998667
Patent No. US20020146747A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                             41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
Best Local Similarity Matches 41; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 41, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: MOD_RES
                                                                                                                                                                                                          RESULT 5
US-09-967-624-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-998-667-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-967-624-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 19
LENGTH: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
```

ä

9; Gaps

쉱

ઠે

```
| Sequence 4, Application US/10160354
| Sequence 4, Application US/20030013107A1
| Sequence 4, Application No. US20030013107A1
| Publication No. US20030013107A1
| GENERAL INFORMATION:
| APPLICANT: Li, Congfen
| APPLICANT: Li, Congfen
| APPLICANT: Rigel Pharmaceuticals, Incorporated
| FILE REFERENCE: 021044-001110US
| CURRENT FILING DATE: 2001-06-07
| NUMBER OF SEQ ID NOS: 4
| SEQ ID NO 4
| SEQ ID NO 4
                                                                                                                                                          APPLICANT: Yang, Jianxin
APPLICANT: Yang, Jianxin
APPLICANT: Yang, Jianxin
APPLICANT: An, Songru
APPLICANT: Thlarik Inc.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Associated With Cancer
FILE REFERENCE: 018781-0083000S
CURRENT APPLICATION NUMBER: US/09/850,948
CURRENT PILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 29
LENGTH: 200
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence:flexible linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: MOD RES
LOCATION: (6)...(200)
OTHER INFORMATION: Gly at positions 6-200 may be present or absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: MOD RES
LOCATION: (6)...(200)
COTHER INFORMATION: Gly at positions 6-200 may be present or absent US-10-160-354-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 77.0%; Score 229.5; DB 10; Length 200; Best Local Similarity 80.4%; Pred. No. 6.7e-12; Matches 41; Conservative 0; Mismatches 1; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.0%; Score 229.5; DB 14; Length 200; 80.4%; Pred. No. 6.7e-12; ive 0; Mismatches 1; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence:poly-Gly OTHER INFORMATION: flexible linker
                                                              JS-09-850-948-29
Sequence 29, Application US/09850948
Publication No. US20030059770Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-850-948-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence:flexible linker NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence:flexible linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Compositions and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (6) ... (200)
; OTHER INFORMATION: Gly at positions 6-200 may be present or absent
US-09-990-940-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MOD_RES

| LOCATION: (6)..(200)

| OTHER INFORMATION: Gly at positions 6-200 may be present or absent

US-09-989-981A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 77.0%; Score 229.5; DB 10; Length 200; 1 Similarity 80.4%; Pred. No. 6.7e-12; 41; Conservative 0; Mismatches 1; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Shan, Bei
APPLICANT: Shan, Bei
APPLICANT: Shan, Bei
APPLICANT: Shan, Bei
APPLICANT: Barnes, Robert
APPLICANT: Barnes, Robert
APPLICANT: Tian, Hu
APPLICANT: Tian, Hu
APPLICANT: Tolarik Inc.
FILE REFERENCE: 018781-007320US
CURRENT APPLICANTION: ABCGS and ABCG8: Compositions and Methods of
FILE REFERENCE: 018781-007320US
CURRENT FILING DATE: 2002-23
FRIOR APPLICATION NUMBER: US 60/252,235
FRIOR APPLICATION NUMBER: US 60/252,235
FRIOR APPLICATION NUMBER: US 60/253,645
FRIOR PRILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.0%; Score 229.5; DB 10; Length 200; 80.4%; Pred. No. 6.7e-12; ive 0; Mismatches 1; Indels 9;
PRIOR APPLICATION NUMBER: US 60/252,841
PRIOR FILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PLILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 60/261,377
PRIOR APPLICATION NUMBER: US 60/279,554
PRIOR PILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver: 2.1
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/09989981A Publication No. US20030049730A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-989-981A-13
                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
```

ä

Gaps

, 6

ij

Gaps

6

```
엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ı,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MOD RES
LOCATION: (6)...(200)
OTHER INFORMATION: Gly residues from position 6 to 200 may be present
OTHER INFORMATION: or absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence:flexible linker
                                                                    Sequence 11. Application US/10026331B
FUBLICATION O. US20030027167A1
FUBLICATION O. US20030027167A1
FAPLICANT: Hitoshi, Yasumichi
APPLICANT: Demo, Susan
APPLICANT: Demo, Susan
APPLICANT: Jenkins, Yonchu
FILE REPERENCE: 021044-001310US
CURRENT APPLICATION NUMBER: US/10/026,331B
CURRENT PILING DATE: 2001-12-21
FRIOR FILING DATE: 2001-08-01
FRIOR FILING DATE: 2001-08-01
FRIOR FILING DATE: 2001-08-01
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGIFF: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRATURE:

NAME/KEY: MOD RES

LOCATION: (6)...(200)

OTHER INFORMATION: Gly at positions 6-200 may be present or absent US-10-026-021-8
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 229.5; DB 14; Length 200;
Pred. No. 6.7e-12;
0; Mismatches 1; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence:poly Gly OTHER INFORMATION: flexible linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.4%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                               US-10-026-331B-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-026-331B-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 8
LENGTH: 200
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (6) - (200)
OTHER INFORMATION: Gly residues from position 6 to 200 may be present
OTHER INFORMATION: or absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hitoshi, Yasumichi
APPLICANT: Hitoshi, Yasumichi
APPLICANT: Hitoshi, Yasumichi
APPLICANT: Pearsall, Denise
APPLICANT: Rigel Pharmaceutical, Incorporated
TITLE OF INVENTION: LETAH: Modulators of Cellular Proliferation
FILE REFERENCE: 021044-000920US
CURRENT APPLICATION NUMBER: US 103/10/160,663
CURRENT FILING DATE: 2002-05-31
PRIOR FILING DATE: 2002-06-37
PRIOR FILING DATE: 2002-0-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 200
TYPE: PRT
FRATURE:
CRANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                          | GENERAL INFORMATION: 02003027/03A1 |
| GENERAL INFORMATION: APPLICANT: Bennett, Mark |
| APPLICANT: Bennett, Mack |
| APPLICANT: Rosel, Alex |
| APPLICANT: Rosel, Alex |
| APPLICANT: Rigel Pharmaceuticals, Incorporated |
| TITLE OF INFORMATION: CD43: Modilators of Mast Cell Degranulation |
| TITLE OF INFORMATION: CD43: Modilators of Mast Cell Degranulation |
| FILE REFERENCE: 021044-001010US |
| CURRENT FILING DATE: 2002-05-31 |
| PRIOR APPLICATION NUMBER: US 60/296,801 |
| PRIOR PLILING DATE: 2001-06-07 |
| NUMBER OF SEQ ID NOS: 3 |
| SOFTWARE: Patentin Ver. 2.1 |
| SEQ ID NO 3 |
| LENGTH: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
PERATURE:
OTHER INFORMATION: Description of Artificial Sequence:poly Gly tag
OTHER INFORMATION: Flexible linker
PERATURE:
                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

77.0%; Score 229.5; DB 14; Length 200;
Best Local Similarity 80.4%; Pred. No. 6.7e-12;
Matches 41; Conservative 0; Mismatches 1; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 14; Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
77.0%; Score 229.5; DB 14
Best Local Similarity 80.4%; Pred. No. 6.7e-12;
Matches 41; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/10161165
Publication No. US20030027763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/10160663
Publication No. US20030040001A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Demo, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MOD_RES
LOCATION: (6)..(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-160-663-3
```

```
1;
OTHER INFORMATION: Description of Artificial Sequence:poly Gly tag
OTHER INFORMATION: flexible linker
PEATURE:
NAME/KEY: MOD RES
LOCATION: (6)..(200)
OTHER INFORMATION: Gly residues from position 6 to 200 may be present
OTHER INFORMATION: or absent
US-10-160-663-3
                                                                                                                                                                                                                      Query Match 77.0%; Score 229.5; DB 14; Length 200; Best Local Similarity 80.4%; Pred. No. 6.7e-12; Matches 41; Conservative 0; Mismatches 1; Indels 9; Gaps
                                                                                                                                                                                                                                                                                                                 ઠે
```

Search completed: September 7, 2005, 13:03:57 Job time : 58 secs

a

This Page Blank (uspic)

```
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

OM protein - protein search, using sw model

7, 2005, 12:47:59 September Run on:

9; Search time 24 Seconds (without alignments) 204.461 Million cell updates/sec

US-09-910-432-19

Perfect score:

Sequence:

51

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters: 283416 seqs, 96216763 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pirl:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

KNA-binding protei hypothetical prote glycine-rich cell hypothetical prote glycine-rich prote transcription fact acp-22 protein - y acp-22 protein - y glydine-rich prote hypothetical prote glydine-rich cell FUS/CHOP mutant fu hypothetical prote glycine-rich RNA-b glycine-rich prote hypothetical prote hypothetical prote GCR 101 protein hypothetical prote probable glycine-r glycine-rich RNA-b glycine-rich RNA-b fus-like protein glycine-rich RNA-b hypothetical prote RNA-binding protei glycine-rich cell glycine-rich hypothetical Description SUMMARIES T04592 S54729 TXNRZG1 T31503 T07381 T04160 T24045 T03583 T20410 T20410 B84777 S49193 S12224 S31415 127005 A26099 S33798 S33799 S12312 S12312 C84470 KNNT2S T120268 T120268 В Query Match Length 199 199 291 892 462 62.6 62.6 62.6 62.4 185.5 185.5 185.5 184.5 184.5 223 212.5 206 206 203 201 198.5 194.5 194.5 194.5 194.5 190.5 190.5 190.5 187.5 186.5 186.5 186.5 Result Š.

prote RNA-b prote prote

embryonic abundant glycine-rich prote calpain (EC 3.4.22 hypothetical prote glycine-rich RNA-b glycine-rich RNA-b glycine-rich prote glycine-rich prote glycine-rich prote glycine-rich prote glycine-rich prote glycine-rich RNA-b fibrillarin (valid hypothetical prote glycine-rich RNA-b fibrillarin (valid	endo-1,4-bera-giuc glycine-rich prote
\$04536 \$01821 CIHUL CIHUL B40505 110479 \$238331 \$20846 A44805 A4805 A32155 A38712 A38712	S14857
<b>44444444444</b>	7 7
157 268 268 1958 162 162 203 220 220 681 148 321 321	157
10000000000000000000000000000000000000	59.6
183 182 182 181.5 181.5 181.1 181 181 181 179 179	177.5
6 6 6 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	4 4

### ALIGNMENTS

H

Jesse,

liana

- Arabidopsis thage 09-Jul-2004 Duesterhoeft, A.	21; 26; Gaps 1; GRDDRRORRGGG 34   :           GSGNGSGRGRGGG 155
RESULT 1 1704592 glycine-rich cell wall structural protein homolog F23E13.120 - Arabidopsis thal glycine-rich cell wall structural protein homolog F23E13.120 - Arabidopsis thal G.Species: Azabidopsis thaliana (mouse-ear cress) G.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 G.Date: 13-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 R.Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; submitted to the Protein Sequence Database, March 1998 A.;Recence number: Z15378 A.;Rocession: T04592 A.;Molecule type: DNA A.;Residues: 1-221 < ABE> A.;Residues: 1-221 < ABE> A.;Cross-references: UNIPROT:065514; EMBL:AL022141 A.;Experimental source: cultivar Columbia; BAC clone F23E13 A.;Note: F23E13.120	74.8%; Score 223; DB 2; Length 221; Similarity 55.8%; Pred. No. 1.4e-11; Conservative 1; Mismatches 7; Indels 26; Gaps GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
RESULT 1  91ycine-rich cell wall structural protein homolog F23E13.1  91ycine-rich cell wall structural protein homolog F23E13.1  91ycine: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_c  C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_c  C.Pate: 21-Apr-1999 #sequence_revision 23-Apr-1999 #text_c  R.Bevan, M.; Hibert, H.; Braun, M.; Holzer, E.; Brandt, A  R.Pereirence number: 215378  A.Pereirence number: 215378  A.Polecule type: DNA  A.Polecule type: DNA  A.Polecule type: UNIPROT:065514; EMBL:AL022141  A.Experimental source: cultivar Columbia; BAC clone F23E13  A.Pole: F23E13.120	74.8%; Score 223; DB 2; 55.8%; Pred. No. 1.4e-11; iive 1; Mismatches 7 .ive 1; Mismatches 7 .
RESULT 1 1704592 glycine-rich cell wall struu C;Species: Arabidopsis thal. C;Date: 23-Apr-1999 #sequen C;Date: 23-Apr-1999 #sequen C;Date: 23-Apr-1999 Requen C;Date: 23-Apr-1999 Requen R;Bevan, M.; Hilbert, H.; B Ribmitted to the Protein Se A;Reference number: 215378 A;Reference number: 215378 A;Residues: 1-21 cBEV A;Residues: 1-22 cBEV A;Genetics: C;Genetics: A;Note: F23E13.120	
RESULT 1 104592 glycine-rich cell wall c;Species: Arabidopais C;Date: 23-Apr-1999 #se C;Accession: T04592 R. Bevan, M.; Hilbert, H submitted to the Protei A,Reference number: 215 A,Accession: T04592 A,Molecule type: DNA A,Residues: 1-21 < ABEV-A A,Cross-references: UNI A,Experimental source: C;Genetics: C;Genetics: A,Map position: 4 A,Note: F23E13.120	Query Match Best Local Matches 4 Oy 1 Db 96 Qy 35

S24729

FNA-binding protein cabeza - fruit fly (Drosophila melanogaster)

NA-binding protein cabeza - fruit fly (Drosophila melanogaster)

N;Alternate names: caz protein

C;Species: Drosophila melanogaster

C;Bate: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 16-Aug-2004

C;Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 16-Aug-2004

C;Accession: S54729

R;Stolow, D. T.; Haynes, S. R.

Submitted to the EMBL Data Library, October 1994

A;Description: Cabeza, a Drosophila gene encoding a novel RNA binding protein, shares how A;Reference number: S54729

A,Cross-references: UNIPROT:027294; EMBL:L37083; NID:g567105; PIDN:AAC41563.1; PID:g567108; Stolow, D.T.; Haynes, S.R.
Nucleic Acids Res. 23, 835-843, 1995
A;Title: Cabeza, a Drosophila gene encoding a novel RNA binding protein, shares homology A;Reference number: S54728; MUID:95223733; PMID:7708500

prote prote

A;Status: nucleic acid sequence not shown

~

```
A;Residues: 1-207 <SAN>
A;Cross-references: UNIPROT:Q43522; EMBL:X95262; NID:g1166449; PIDN:CAA64559.1; PID:g1166
A;Experimental source: cultivar UC82b; fruit
  glycine-rich cell wall structural protein 1 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-285 <WIL>
A;Cross-references: UNIPROT:Q9U2U0; EMBL:AL117204; PIDN:CAB55137.1; CESP:Y116A8C.35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: T07381

R;Santino, C.G.; Stanford, G.L.; Conner, T.W.
Plant Mol. Biol. 33, 405-416, 1997

A;Title: Developmental and transgenic analysis of two tomato fruit enhanced genes.

A;Reference number: Z16000; MUID:97201476; PMID:9049262
                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glydine-rich protein Tfm5 - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein Y116ABC.35 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31503
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                109 dsadadadadadadasagasasayayayayakadadadadadadadadadada 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 GGGGGGGGGYGSGGGWGGGGGRD----RDRGGWGGGGGGRGYGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21
                                                                                                                                                                                                                                                                         21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                         Length 285;
                                                                                                                                                                                         Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Indels
                                                                                                                                                                                       69.1%; Score 206; DB 1;
ilarity 72.5%; Pred. No. 2.5e-10;
Conservative 1; Mismatches 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.1%; Score 203; DB 2;
ilarity 76.5%; Pred. No. 6.4e-10;
Conservative 0; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 201; DB 2;
Pred. No. 7.4e-10;
0; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: T31503
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;McMurray, A.
submitted to the EMBL Data Library, October 1999
A;Reference number: 221041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: hydroxyproline-rich glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: clone Y116A8C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.4%;
ilarity 70.6%;
Conservative (
F;24-165/Product: glycine-r
F;30-55/Region: repeat R1
F;56-62/Region: repeat R2
F;62-92/Region: repeat R1
F;93-99/Region: repeat R2
                                                                                                     F;100-131/Region: repeat R1
F;132-138/Region: repeat R2
F;139-160/Region: repeat R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                          Local Similarity
les 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: CESP: Y116A8C.35
A; Introns: 31/3; 143/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 39
                                                                                                                                                                                           Query Match
                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                    r31503
                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q18444; EMBL:U58755; PIDN:AAB00696.1; GSPDB:GN00022; CESP:C3 A;Experimental source: strain Bristol N2; clone C34D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: UNIPROT:P25074; EMBL:X53596; NID:g20246; PIDN:CAA37665.1; PID:g20247
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                      ω,
                                                                                                                                                                                                                                                                                                                                   214 GGGGGGGGRGGRGGRRGGGGGGGGGRRPD----RGGGGGGRGGGGGRYDRGGGG
                                                                                                                                                                                                                                                                                            hypothetical protein C34D4.11 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Accession: T29282 R;Du, Z.; Le, T.T. Submitted to the RMBL Data Library, May 1996 A;Description: The sequence of C. elegans cosmid C34D4.
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gandedendedengedengededengengengengengengengengengen 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
                                                                                                                                                                                                                                                   17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                             2; Length 404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 136;
                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 206; DB 2; Length 13
Pred. No. 2.2e-10;
0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Gene: grp-1
C;Superfamily: glycine-rich cell wall structural protein 1
C;Keywords: cell wall; duplication; structural protein
F;1-23/Domain: signal sequence #status predicted <SIG>
                 A;Residues: 118-203;273-310 <STW>
A;Cross-references: EMBL:L37083
C;Genetics:
A;Gene: cabeza
A;Cross-references: FlyBase:FBgn0011571
C;Superfemily: ribonucleoprotein repeat homology
C;Keywords: RNA binding
F;120-195/Domain: ribonucleoprotein repeat homology <RRM>
                                                                                                                                                                                                          Score 212.5; DB 2;
Pred. No. 1.5e-10;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-136 <DUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: CESP:C34D4.11
A;Map position: 4
A;Introns: 20/1; 66/1; 98/1; 116/1
C;Superfamily: Arabidopsis glycine-rich protein 3
                                                                                                                                                                                                             71.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.1%;
ilarity 74.5%;
Conservative
                                                                                                                                                                                                                                                      43; Conservative
                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 43; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
ee 38; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                     GGG 271
                                                                                                                                                                                                                                                                                                                                                                          49 GGG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 38
                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                            ଚ
                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
```

ä

us-09-910-432-19.rpr

```
A,Cross-references: UNIPROT:Q7XJP7; GB:AE002093; NID:g4895201; PIDN:AAD32788.1; GSPDB:GNC C;Genetics: A,Gene: Ax2g37830 A;Gene: Ax2g37830 A;Map position: 2 C;Superfamily: Arabidopsis glycine-rich protein 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gispecies: Oryza sativa (rice)
Cibate: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
Cibate: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
Cibatession: T03583
Rilee, M.C.; Kim, C.S.; Yi, B.Y.; Lee, J.S.; Eun, M.Y.
Rilee, M.C.; Kim, C.S.; Yi, B.Y.; Lee, J.S.; Eun, M.Y.
A; Description: Isolation and characterization of RNA-binding glycine rich protein of ric.
A; Reference number: 214958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-165 <LLBS>
A;Cross-references: UNIPROT:024184; EMBL:AF009411; NID:g2267592; PIDN:AAB63589.1; PID:g2;
A;Experimental source: cv. Milyang 23
C;Superfamily: glycine-rich RNA-binding protein; ribonucleoprotein repeat homology
P;9-76/Domain: ribonucleoprotein repeat homology <RRM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: T49109
Wi, Wedler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mr Submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:065450; EMBL:AL022140; GSPDB:GN00062; ATSP:AT4g22020
A;Experimental source: cultivar Columbia; BAC clone F1N20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - DRRQRRRGGGGGGGG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.Alternate names: protein AT4922020
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 165;
                                                                                                                                                                                                                                                             Length 106;
                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 4
C;Superfamily: Phaseolus glycine-rich cell wall protein 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 65.3%; Score 194.5; DB 2; Best Local Similarity 67.2%; Pred. No. 2.1e-09; Matches 41; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                         65.3%; Score 194.5; DB 2 ilarity 55.7%; Pred. No. 1.5e-09; Conservative 0; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycine-rich protein - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glycine-rich RNA-binding protein - rice
                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGGGGGGGGGGGGGGGRGRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 GGGGGGGG 51
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-396 <BEV>
A;Residues: 1-106 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: ATSP: AT4g22020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: T03583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 G 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: T49109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 G 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein At2g37830 [imported] - Arabidopsis thaliana hypothetical protein At2g37830 [imported] - Arabidopsis thaliana (C) Species Arabidopsis thaliana (mouse-ear cress) (C) Species 2. Pab-2001 #sequence_revision 02-Peb-2001 #text_change 09-Jul-2004 (C) Accession: P84797 (C) Accession: Paper Accession: Paper Accession: Paper Accession: P84797 (C) Accession: P84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-1226 <WIL>
A;Cross-references: UNIPROT:Q21835; EMBL:Z68008; PIDN:CAA92000.1; GSPDB:GN00028; CESP:RC
A;Experimental source: clone R08B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q98937; EMBL:U47276; NID:g1546783; PIDN:AAB08467.1; PID:g154
C;Superfamily: fork head DNA-binding domain homology
F;143-234/Domain: fork head DNA-binding domain homology <FHD>
                                                                                                                                                                                                                                                                                                                                                                                expression of transcription fact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: X
A;Introns: 53/2; 113/1; 152/3; 204/3; 272/1; 354/1; 389/3; 714/3; 839/3; 877/1; 960/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                               C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 16-Aug-2004
C;Accession: S71795
R;Yusas, J.; Hirano, S.; Yamagata, M.; Noda, M.
Nature 382, 632-635, 1996
A;Title: Visual projection map specified by topographic expression of transc: A;Reference number: S71794; MUID:96338226; PMID:8757134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aypothetical protein R08B4.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24045
B;White, S.
Submitted to the EMBL Data Library, November 1995
A;Reference number: Z19834
A;Accession: T24045
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T24045
A;Status: preliminary; translated from CB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGGGGGGGGGGGGGGGRPPSRGGPQKAAAAGGGGAGGGGGGGGGAGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.6%; Score 198.5; DB 2; Length 440; 66.1%; Pred. No. 2e-09; ive 1; Mismatches 13; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-440 <YUA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.4%; Score 195; DB 2; ilarity 66.7%; Pred. No. 7.7e-09; Conservative 0; Mismatches 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 66.1
nes 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
hes 34; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Gene: CESP: R08B4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
```

ų,

Drosophila genes

3,

12; Gaps

48

```
173 GGGGGGFGGRGGRGGGRGGGGRGGGGFRGGAGRNGGGGGGGGGFNRGRGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;&peciès: Tenebrio molitor (yellow mealworm)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
     16-Peb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GGGGGGAAGGLLEGGGGFEEYGHRSRGSIIGLSRGIEIGRHYGGGGGGGGGEGEEREL
                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q9W2L8; EMBL:X71975; NID:g510508; PID:g510509
C;Genetics:
A;Gene: FlyBase:anon-Pen101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P26968; EMBL:X60455; NID:g10750; PID:g10751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: S16063
R; Bouhin, H.; Charles, J.P.; Quennedey, B.; Delachambre, J.
submitted to the EMBL Data Library, July 1991
A; Description: Molecular cloning of a glycine-rich cuticular protein.
A; Reference number: S16063
A; Rccession: S16063
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 64.1%; Score 191; DB 2; Length 239; Best Local Similarity 65.1%; Pred. No. 5.1e-09; Matches 41; Conservative 0; Mismatches 10; Indels :
                                           R; Parchment, C.; Hughes, D.M.; Lloyd, P.; Flavell, A.J. submitted to the EMEL Data Library, May 1993
A; Description: A variety of different glycine repeats in A; Reference number: S49192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 190.5; DB 2;
Pred. No. 4.9e-09;
1; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: FlyBase:FBgn0011824
C;Superfamily: Phaseolus glycine-rich protein 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 RGG---GGGGGGGGGGGG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGGGG--GG---GGGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 63.9%;
Best Local Similarity 50.0%;
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein - yellow mealworm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-199 <BOU>
                                                                                                                                                                        A, Accession: S49193
A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-239 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 GGG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 GGG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q9SIH2; GB:AE002093; NID:g4678224; PIDN:AAD26969.1; GSPDB:GN
C;Genetics:
C;Genetics:
A;Gene: Arg36120
A;Map position: 2
C;Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q93424; EMBL:Z81053; PIDN:CAB02877.1; GSPDB:GN00023; CESP:Ed
A;Experimental source: clone E02A10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein At2g36120 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84777
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84777
                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ï
                                                                                                                                                                                                                                                                                                      hypothetical protein B02Al0.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T20410
R;Thomas, K.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                   21
                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.1%; Score 194; DB 2; Length 396; 68.6%; Pred. No. 4.2e-09; ive 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 192; DB 2; Length 255;
Pred. No. 4.4e-09;
1; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 64.6%; Score 192.5; DB 2; Local Similarity 72.5%; Pred. No. 5.4e-09; Nes 37; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          849193
GCR 101 protein - fruit fly (Drosophila melanogaster)
C,Species: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-385 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: CESP:E02A10.2
A;Map position: 5
A;Introns: 32/1; 72/1; 85/1; 122/1; 133/1; 220/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.4%;
Local Similarity 64.9%;
les 37; Conservative
                             Best Local Similarity 68.6
Matches 35, Conservative
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
                                                                                                                 ઠે
                                                                                                                                                                용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઢ
```

```
Search completed: September 7, 2005, 13:00:51
Job time : 25 secs
81 RGGGLELGGGGGGGGGGGGGEG 104
```

80

-----GGGGGGGGRGRDDRRORR

Indels